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protein NPR1 (NPR1) mRNA, complete
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Cao, H., Glazebrook, J., Clarke, J.D., Volko, S. and Dong, X. The Arabidopsis NPRI gene that controls systemic acquired resistance encodes a novel protein containing ankyrin repeats 97148688
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Cao.H., Glazebrock,J., Clarke,J.D., Volko,S. and Dong,X.
Direct Submission
Submitted (30-OCT-1996) DCMB Group, Botany, Duke University, LSRC
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1 (bases 1 to 2154)

K Roesema, E., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Shinn, P., Banh, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, S.X., Miranda, M., Narusaka, M., Nguyen, M., Chodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana Atlg64280/F15H21_6 mRNA linear PLN 20-AUG-2001 AY050455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-AUG-2001) Salk Institute Genomic Analysis Laboratory (SIGnAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                             1741 AGACACTAAAGAAGGCCTTTAGTGAGGACAATTTGGAATTAGGAAATTCGTCCCTGACAG 1800
                                                                                                               ATTCGACTTCTTCCACATCGAAATCAACCGGTGGAAAGAGGTCTAACCGTAAACTCTCT 1860
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BONTAAVKLELKEIAKDFYSTSVEPSVYVLALVYS SSRVRPPPFKGVSECADENCCHVAC
RPAVDFMLEVLYLAFFKIPELITIYOKHLLDVVDKVVIEDTLVILKLANTGGRACMK
LLDRCKEIIVKSNVDMVSLEKSLPEELVKEIIDRRKELGLEVPKVKKHVSNVHKALDS
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VAAMKKEPOLILISLILEKGAGASEATLEGRTALMIAKOATMAYBCNNIPPEOCHHSLKGR
LOCETILEDOEDKREQIPPDVPPSFAVARDELKMILLDLENKVALAQRIEPPTAQAAMEI
AEMKGYCEFTYSLEPPRIJGTRRSPGVK APFRILEEHOSKLKALSKTVEGKREF
PRCSAVLDQIMNCEDLTQLAGGEDDTAEKRLOKKQRYMEIQETLKKAFSEDNILELGN
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                                                                                                                              The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDRAS: Koesema, E., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Shinn, P., Banh, J. Bowser, L., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G. Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Ondera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Southwick, A., Pang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satcu,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                 Koesema, E. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as Pls.

Location/Qualifiers

1. 2114

/organism="Arabidopsis thaliana"
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/note="transcription factor inhibitor I kappa
/codon_start=1
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/chromosome="1"
/clone="RAFL07-16-K16(R13446)"
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/protein_id-"AAK91469.1"
/db_xref-"GI:15215850"
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llarity 99.9%; Pred. No. 0;
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Uknes,S.Joseph, Hunt,M.Denise, Steiner,H. and Ryals,J.Andrew.
Altered forms of the NIM1 gene conferring disease resistance
       1507 TCGCCGAAATGAAGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCTGACCGTCTCA
                                                              1501 CTGGTACGAAGAACATCACCGGGTGTAAAGATAGCACCTTTCAGAATCCTAGAAGAGC
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100.0%; Pred. No. 0;
Live 0; Mismatches
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1 (bases 1 to 2011)
Uknes, S. Joseph, Hunt, M. Denise, Steiner, H. and Ryals, J. Andrew.
ATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATATATCCCGGAGCAATGCAAG
                                               ATTCCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAATTGAAGATGACGCTG
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Lin,X., Kaul,S., Town.C.D., Benito,M.-I., Creasy,T.H., Haas,B.J., Wu.D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M. Unpublished
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Town,C.D. and Kaul,S.

Direct Submitsation
Submitted (19-JAN-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org on Jan 19, 2001 this sequence version replaced gi:12280769.

Address all correspondence to:at@tigr.org
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/gene="F15H21.17"
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<887. .>1915
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Direct Submission
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                                                                                                                                                                                                                                           SPEFPINPRNPGAPVIPRNNPPVFPGNPRSMGPPGFPGIGGPPGFFFTFFFGGGGTG
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GSVLGFHC"
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 sa putative non-autonomous DNA transposon - a consensus."
complement(3199...3435)
/rpt_family="SIMPLEGUY1|SIMPLEGUY1 ss a
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1|SIMPLEGUY1|s a putative non-autonomous DNA transposon - a consensus."

complement(3384. 3494)

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complement(3384. 3457)

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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensus."
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 SIMPLEGUY1 is a
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is
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complement(4109.
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12686. .12786,13367. .13702,13835. .13925,14904. .15298,
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ESIONASNSGNNDLENOYTIEFOKRGLPHAHILLEMHPTSKLSTABDTDKVLTAEI
PDKKKREBLAAVKROMIHGPGGVGHPNSPCMENGKCKKYFPKSYSDTTKVDNDGFPV
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LKIYGTDYTTKDGTGVRDYIHVVDLADGHICALQKLDDTEIGCEVYNLGTGKGTTVLE
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complement(10465. .10537)

/gene="60083.tmv-Ala-1"

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/protein_id="AAG51717.1"
/db_xref="G1:12323478"
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/protein_1d="AAG51706.1"
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                                      ATGGTATACAGATTTGTAATATATTTTATGTACATCAACAATAA
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Uknes, S. Joseph, Hunt, M. Denise, Steiner, H.
Altered forms of the NIMI gene conferring
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Sequence 1 from patent US 5986082.
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1. .5655
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Best Local Similarity 87.5%;
Matches 2088; Conservative
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qq		Db 4375 CGTCTCACTGGTACGAAGAGAACA
οy	09	Db 4435 GAAGAGCATCAAAGTAGACTAAAA
qq	55 ACCATCTGCATTAAGCTATGGTTACACATTCATGAATATGTTCTTACTTGAGTACTTGTA	Qy 1593
Q P	650TCARAGGCACTTATTGGACGTTGTAGACAAGTTGTTATAGAGACACATTG /01 3415 TTTGTATTCAGAGGCACTTATTGGACGTTGTAGACAAGTTGTTATAGAGACACACATTG /01 3415 TTTGTATTCAGAGGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTG 3474	
۶ و د	702 GTTATACTCAAGCTTGCTAATATATGTGGTAAAGCTTGTATGAACCTATTGGATAGATGT 761 	
3 8	2 AAAGAGATTATTGTCAAGTCTAATGTAGATAGGTTAGTCTTGAAAAGTCATTGCCGGAA	Qy 1623 TGTTCGGCAGTGCTCGACCAGAT:
Qy Qy	5 AAAGAGATTATTGTCAAGTCTAATGTAGATATGGTTAGTCTTGAAAAGTCATTGCCGGAA 5559 2 GAGCTTGTTAAAGAGATAATGATAGACGTAAAGAGCTTGGTTTGGAGGTACCTAAAGTA 881 1111111111111111111111111111111111	Qy 1683 GAAGACGACACTGCTGAGAAACG3
oy o		Qy 1743 ACACTAAAGAAGGCCTTTAGTGA(
8 & 6	### CTCGGAATGFACATAAGGCACTTGACTCGGATGATATIONSTINATICANS AAGAGGATCACAATCTAGATGATGGGTGTGCTTTCATTTCGCTGTT	OY 1803 TCGACTTCTTCCACATGAAATC.
8 % B	GCATATTGCAATGTGAAGACGCCAACAGATCTTTAAAAACTTGATCTTGCCGTGTCAAC 106	1863
8 8 8		1923
8 8 8	TTGATACTA TGATACTA	1983
oy do	2 2	QY 2043 AATGGTAACAGATTTGTAATAL DD 5035 AATGGTATACAGATTTGTAATAT
oy Og	1242 CAATGCAAGCATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGACAAA 1301 	RESULT 7 ATU87794 LOCUS DESTAURTION ATU87794 FEB 1 and
oy Op	1302 CGAGAACAAATTCCTAGAGATGTTCCTCCCTCTTTGCAGTGGCGGCCGATGAATTGAAG 1361 	Additional Control Momolog (niml) gene U87794 U87794.1 GI:191691
oy Og	1362 ATGACGCTGCTCCGATCTTGAAAATAG	NEIWONGE thate cress. ORGANISM Arabidopsis thaliana Eukaryota; Viridiplan
οy		Spermaccpnyca; Magnor Rosidae; eurosids II; REFERENCE 1 (bases 1 to 5655)
Dp	5 AATTAAATTTATGTCCTCTCTATTAGGAAACTGAGTGAACTAATGATAACTATTGT 425	
Qy Dp	1388	
S d	1434 ATGGAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCTGAC 1493 	MEDLINE 97246324 REFERENCE 2 (bases 1 to 5655) AUTHORS Ryals,J., Weymann,K.,
οy	1494 CGTCTCACTGGTACGAAGAAACATCACCGGGTGTAAAGATAGCACCTTTCAGAATCCTA 1553	Steiner, n. T., Journal Uknes, S. TITLE Direct Submission

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5655 bp DNA linear PLN 25-MAY-1997 transcription factor inhibitor I kappa B complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tae; Streptophyta; Embryophyta; Tracheophyta; iophyta; eudicotyledons; core eudicots; Brassicales; Brassicaceae; Arabidopsis.
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                                                  AGCGCTTTCTAAAACCGGTATGGATTCTCACCCACTT 4494
                                                                                                     CAAAACTAAATGATCTTTAAACATGGTTTTGTTACT 4554
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on,J., Delaney,T.P., Jesse,T., Vos,P. and
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 3355 ACCATCTGCATTAAGCTATGGTTACACATTCATGAATATGTTCTTACTTGAGTACTTGTA
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ted (29-JAN-1997) Fungicides, Novartis
Research Triangle Park, NC 27709, USA
Location/Qualifiers
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/gene="nim1"
                                                                      thaliana"
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Pred. No. 0;
                                                                    /organism="Arabidopsis
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join(2754. .3347,3427.
2787. .4866
                                                                                      /cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="1"
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586 ATTTCATGTTGGAGGTT 122 ATTTCATGTTGGAGGTT 646 TCTATCAGAGGCACTTA 182 TCTATCAGAGGCACTTA 706 TACTCAAGCTTGCTAAT 242 TACTCAAGCTTGCTAAT 76 AGATTATTGTCAAGTT 76 AGATTATTGTCAAGTT 826 TTGTTAAAGAGATATT 826 TTGTTAAAGAGATAATT 827 ATTGAAAGAGATAATT 828 AACATGTCTCGAATGTA 826 TTGTTAAAGAGATAATT 827 ATTGAAAGAGATAATT 828 ATTGAAAGAGATAATT 829 ATTGAAAGAGATAATT 820 ATTGCAATGTGAATGTA 106 GGAATCCGAGGATATT 1126 TACTATCTCTAATGGAATATT 1126 GGAATCCGAGGATATT 1126 TACTATCTCTATTGGAAGATATT 1126 TACTATCTCTATTGGAAGAGACT 106 GGAATCCGAGGGATATT 1126 TACTATCTCTATTGGAAGATATT 1126 TACTATCTCTATTGGAAGATATT 1126 TACTATCTCTATTGGAAGATATT 1126 TACTATCTCTATTGGAATATT 1127 TACTATCTCTATTGGAATATT 1127 TACTATCTCTATTGGAATATT 1127 TACTATCTCTATTGGAATATT 1127 TACTATCTCTATTGGAATATT 1128 TACTATCTCTATTGGAATAT 1128 TACTATCTCTATTGGAATAT 1129 TACTATCTCTATTGGAATAT 1121 TACTATCTCTATTGGAATAT 1121 TACTATCTCTATTGGAATAT 1121 TACTATCTCTATTGGAATAT 1121 TACTATCTCTATTGGAATAT 1127 TACTATCTCTATTGTATTGGAATAT 1127 TACTATCTCTATTGTATT 1127 TACTATCTCTATTGTATT 1127 TACTATCTCTATTGTATT 1127 TACTATCTCTATTGTATT 1127 TACTATCTCTATT	62 TACTATCTATTGGAA 1186 CACTCATGATCGCAAAA 126 CACTCATGATCGCAAAA 126 CAAGCATTCTCTCAAA 1306 AACAAATTCTTCAAAA 1366 CGCTGCTCGATTGAA 1366 CGCTGCTCGATTGAA 1426 AACAATTCTTGAA 1466 AACTGCAACTTTGAA 1486. AGCTGCACTCTTCAA 1606 AACGTTCTTCACTTGAA 1606 AACGTTCTTCACTTGAA 1606 AACGTTCTTCACTTGAA 1606 AACGTTCTTCCCGCGCATTGAA 1606 AACGTTCTTCCCGCGCATTGAA 1606 AACGTTCTTCCCCGCGCATTGAA 1606 AACGTTCTTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
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Qy 766 AGATTATTGTCAAGTCTAATGTAGATATGGTTAGTCTTGAAAAGTCATTGCCGGAAGAGC 825	0y 1186 CACTCATGATCGCAAAACAAGCCACTATGGCGGTTCAATAATATATAT	RESULT 11 AR087507 LOCUG DEFINITION Sequence 15 from patent US 5986082. ACCESSION AR087507 GI:10014270 VERWORDS SOURCE ORGANISM UNKnown. GICLASSIFIED AUTHORS GICHARORS
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	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 104738) Bevan, M., Rose, M., Hempel, S., Entian, KD., Hoheisel, J., Mwwes, H. W., Mayer, K. F. X., and Schueller, C.	Unpublishe 2 (bases EU Arabido	che Max-Planck-Institu 182152 Martinsried, FRC C@mips.biochem.mpg.de	, Cambridg, rwich, UK, lled	annotatio viewed at	/organism="Arabidopsis thaliana" /variety="Columbia" /db_xref="Laxon:3702" /chromosome="4"	86261 /gene="F20B18.10" /number=1 join(86261,380514,606708,761896,10061175)	tum ciliare possible ne pSUB C, PID:9549984	/product-"possible apospory-associated like protein (fragment)" /protein_ld="Cab39655.1" /db_xref="G1:453819"	/translation="MFFMEVQYSNTGPLPSHGFVRQRFWEVETKPPPLPSLSTAHVDL IVRSSNEDLKIUPHRKEYRLAKJGHDGDLTLTSTRYKNTDVTRFNFTFAHPHPARVSN ISEHVEGLHNLDYLLOGOKNRTRFTPHRKYITFRAGSITKKHTLGKKLDRLXLSTPD QLRIVDHKKKKTIVVHKEGGVDAVVWNPPMDKKVSDLGVEDYKRFVTVESSAAVAKPITV		/gene="F20B18.10" /number=1 38054 /gene="F20B18.10"	/number=2 on 515605 /gene="F20818.10" /number=	606. /gene /numb	/gene /pumb	/b1896 /gene="F20B18.10" /number=4 nn 8971005	/gene="F20B18.10" /number=4 10061175
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9598. .9725,9822. .9960,10052. .10149,10227. .10296,
10389. .10478))
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protein LAP - Drosophila melanogaster, PID:94160434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 282; Gaps
                                                                                                                                    /note="similarity to other hypothetical proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 104738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IXYVGCNFGYHDIATDTTINFYTHSNVPLRSTEFPYWPLPLS 5184. :5228 /gene="F20B18.40"
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Pred. No. 2.8e-166;
0; Mismatches 426;
                                                                                                                                                                                                                                          /product="putative protein"
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/number-
                                                                                                                                                                             Arabidopsis thaliana"
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6850. 7171
/gene="F20B18.40"
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/gene="F20B18.50"
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6046. .6773
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complement(7570.
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/gene="F20B18.40"
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                              /gene="F20B18.40"
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64.8%;
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5455. .60
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Best Local Simi.
Matches 1304;
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Anabaena sp., Pir2:D34443"
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/gene="F220818.30"
/note="similarity to other hypothetical proteins
Arabidopsis thaliana"
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/gene="F20B18.10"
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1345 GGGCGGATGGATTGGAGTTGGTGTTTTAAAAAAA 1345 GGGCGATGGATTGGAGTTGGTGTTTTAAAAAAAA 1346 TCCARAGGATTGGATTGGGTTGGTTTTAAAAAAAAA 1346 TCCARAGGATTGGATTTGGGTTAGGAAATGAAAATGATGAATGA

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join(13985. 114010,14239. 14669,14761. 14921,15016. 15219,
join(13980. 15595,15645. 16227)
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/note="EST GB:E14385 in 5' untranslated region
strong similarity to calmodulin-binding protein (TCB60) -
Nicotianatabacum, PID:g16898548
contains EST gb:F14386, F14385, N96168, N96141"
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Vakroplptpspkpliyopppyopptgsfeqoeldphntvrgglglpplvwdvkias
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Gdgwcghytqivwretrrlgcarvvcengagvfitcnydppgnyygekpy"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="strong similarity to gene PR-1 protein - Medicago truncatula, PIR2:S47171 contains Extracellular proteins SCP/Tpx-1/Aq5/PR-1/Sc7 signatures AA166-176; Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 contains EST gb:AA712715, N65358"
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Contains Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signatures AA147-157; Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signatures AA173-184 contains EST gb:226548, AA586201, AA712838, AA712715"
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complement(join(10710. .11074,11485. .11752))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(11075, .11484)
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complement(10710. .11074)
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                                                                                                                                                                                        .8133)
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7278. .7370,7494. .7733,7782. .7882,7945. .8042,8134. .8444))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .8444))
E d (bases 1 to 196286)

S EU Arabidopsis sequencing, project.

Direct Submission

Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer

Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer

Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, E-mail:

lemcke@mips Jbiochem.impg.de_mayre@mips biochem.mpg.de Project

Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge

Laboratory John Inness Centre, Colney Lane, NR4 7UJ Norwich, UK,

E-mail: michael.bevandebsrc.ac.uk

Information on performance of analysis and a more detailed

annotation of this entry and other sequences of chromosomes 3, 4

and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/

this fragment has an overlap with ATCHRIV63 at the 5' end and an

overlap with ATCHRIV65 at the 3' end.
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TEMOI SPFTLY STSTFTAGY SYNCTLTTALPHNPOAQ PPOYDALASY STVPLSQFPEFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITCTACAGCGACGCTAAGCTIGTICTCTCCGACGGCCGGGAAGTTTCTTTCCACCGGTG 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 196286;
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ΟŊ	650		687
q	125513		125572
Qy Dp	688 125573	TAGAGGACACATTGGTTATACTCAAGCTTGCTAATATATGTGGTAAAGCTTGTATGAAGC '	747 125632
QY Dp	748 125633	TATTGGATAGATGTAAAGAGATTATTGTCAAGTCTAATGTAGATATGGTTAGTCTTGAAA	807 125692
QY Db	808	AGTCATTGCCGGAAGAGCTTGTTAAAGAGATAATTGATAGACGTAAAGAGCTTGGTTTGG	867
Qy	868 125753	4 (2	27
Q <u>y</u> Db	928 125813	TTGAGTTAGTCAAGTTGCTTTTGAAAGAGGATCACACCAATCTAGATGATGCGTGTGCTC ! 	987 125872
Qy	988 125873	TTCATTTCGCTGTTGCAAATGTGAAGACCGCAACAGATCTTTAAAACTTGATC 1	1047 125932
QY	1048 125933	TTGCCGATGTCAACCATAGGAATCCGAGGGATATACGGTGCTTCATGTTGCTGCGGATGC	1107 125992
QY Db	1108 125993	GGAAGGAGCCACAATTGATACTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAA 1 	1167 126052
Qy Db	1168 126053	CTTTGGAAGGTAGAACCGCACTCATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTA 1 1 1 1 1 1 1 1 1 1	1227 126112
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1684 AAGACGACACTGCTGAGAAACGACTACAAAAGAAGCAAAGGTACATGGAAATACAAGAGA 1743
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SVANLCNKSCMKLLERCLDMVVRSNLDMTTLEKSLPPDVIKOIIDARLSIGISPENK
GEPRKHVRRTHRALDSDDVEVRMLLTFGGTVHNDAFALHTAYBHCDSKITTELLDLA
LADVNHRNPRGYTVHIAALRARREPKIIVSLLTKGARRADVTFDGRAVYOISKETKO
DYFGVTEEGKPSPKDRLCIEILEQAERRDPQLGEASVSLAMAGESLRGRLIXLENNVA
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Monocotyledonous plant genes and uses thereof
Patent: WO 0166755-A 15 13-SEP-2001;
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/db_xref="taxon:4565"
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Best Local Similarity 57.3%;
Matches 688; Conservative
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October 7, 2002, 21:14:44; Search time 227.819 Seconds (without alignments) 15856.428 Million cell updates/sec
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Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                        1736436 segs, 858457221 residues
                                                                        - nucleic search, using sw model
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries N_Geneseq_032802:*

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ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Arabidopsis thalia	A. thaliana NIM-1	A. thaliana NIM-1	Non-inducible immu	Arabidopsis thalia	A. thaliana NIM-1	A. thallana non-in	Arabidopsis thalia	A. thaliana non-in
TD TD	AAV16851	AAV46274	AAV46275	AAV43661	AAC37765	AAV46273	AAV43659	AAV04632	AAV43658
DB	19	19	19	19	21	19	19	19	19
% Query Match Length DB	2104	2011	2011	2011	2024	5655	5655	5655	9919
% Query Match	100.0	95.5	95.4	95.4	94.8	83.7	83.7	83.7	83.7
Score	2104	2009.4	2006.2	2006.2	1993.6	1760	1760	1760	1760
Result No.	Н	7	3	4	5	9	7	8	6 ي

Arabidopsis thalia Arabidopsis thalia	A. thallana C-term	n-inducible	A. thaliana N-term		A. thaliana C- and	Non-inducible immu	B. napus NIM1 homo	A. thaliana NIM1 h	A. thaliana NIM1 h	A. thaliana NIM-1	õ	L. esculentum NIM1	N. tabacum NIM1 ho		B. vulgaris NIM1 h	Rice NPR1 homologu	Rice putative nega	cDNA sequence enco	ă	S. tuberosum NIM1		B. napus NIM1 homo	N. tabacum NIM1 ho	Nph1	Rice Nph1 protein	cDNA sequence enco	Rice putative nega	DNA sequence encod	L. esculentum NIM1			rabidopsis	ris NI	H.annuus NIM1 homo
AAV04631 AAV16850		AAV43663	AAV46276	AAV43662	AAV46278	AAV43664	AAA97192	AAA97202	AAA97233	AAV46279	AAV43665	AAA97191	AAA97190	AAV16852	AAA97229	AAC81457	AAA61047	AAH43382	AAH43384	AAA97219	AAA97211	AAA97225	AAA97234	AAC84340	AAC84339	AAH43381	AAA61048	AAH43377	AAA97215	AAC68800	AAA97193	AAC46995	AAA97216	AAA97230
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NPR1 gene; acquired resistance; disease; plant pathogens; bacteria; mycoplasma; fungi; insects; nematodes; viruses; viroids; transgenic; ds.
                                                                                                                                                                    /product= acquired resistance protein
/note= NPR1 gene
                                                                    Arabidopsis thaliana acquired resistance gene NPR1.
                                                                                                                                        Location/Qualifiers
93..1874
                 AAV16851 standard; cDNA; 2104 BP
                                                                                                                                                                                                                                                97US-0046769.
96US-0023851.
97US-0035166.
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                                                   (first entry)
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                                                                                                                        Arabidopsis thaliana.
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09-AUG-1996;
10-JAN-1997;
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                                                       New isolated plant acquired resistance polypeptide gene - useful for, e.g. producing plants with increased resistance to pathogens such as bacteria
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1741 AGACACTAAAGAAGGCCTTTAGTGAGGACAATTTGGAATTAGGAAATTCGTCCCTGACAG 1800
                                                                                                                                               This cDNA sequence encodes the NIM-1 protein from Arabidopsis thaliana. This protein is used in a method resulting in the protection of an immunomodulated plant having a first level of resistance and involves treatment with at least 1 microbicide that confers a second level of
                                                                                                                                                                                                                                                                                                                                                         NIM-1; noninducible immunity; systemic acquired resistance; SAR; pathogen; disease; protection; immunomodulated; plant; cereal; fruit; vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.
                             TTTCATGATGACTGTAACTGTTTATGTCTATCGTTGGCGTCATATAGTTTCGCTCTTCGT
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resistance, such that the plants have a third level of resistance greater than the sum of the first two levels. The method can be applied to a wide variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect against viruses, fungi, bacteria, insects and nematodes. The method provides a high level of resistance and allows a reduction in the amount of micobicide used. Since the process involves two different methods of protection, it is unlikely that the pathogen will develop resistance to the treatment.
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This sequence encodes a variant NIM-1 protein from Arabidopsis thaliana. This protein is used in a method resulting in the protection of an immunomodulated plant having a first level of resistance and involves treatment with at least 1 microbicide that confers a second level of resistance, such that the plants have a third level of resistance greater than the sum of the first two levels. The method can be applied to a wide variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect against viruses, fungi, bacteria, insects and nematodes. The method of micobicide used. Since the process involves two different methods of protection, it is unlikely that the pathogen will develop resistance to
                                                                                                                                                                                 NIM-1; noninducible immunity; systemic acquired resistance; SAR; pathogen; disease; protection; immunomodulated; plant; cereal; fruit; vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.

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No. 0;
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             1981 ACAATTTGAACCAATGGTATACAGATTTGTA 2011
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/note= "wild type TCG
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2031 ACAATTTGAACCAATGGTATACAGATTTGTA
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/*tag= a
/product= NIM-1
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                                                                                                                                                            thaliana NIM-1 cDNA variant
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/note= "wild t
217..219
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96US-0034378
                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                        Arabidopsis thaliana.
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P-PSDB; AAW64436.
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Best Local Similarity
                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2011 BP;
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the treatment.
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                                                                                     AAV46275
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Tue Oct

OY 1131 TCTCTATTGGAAAAAGGCGAGTGCATCAGAAGCAACTTTGGAAGGTAGAACCGCACTC 1190	1251 CATTCTCTAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGAAGAAACAA 	1311 ATTCCTAGACANGTTCCTCCTCTTTTGCAGTGGCGGCCGATCAATTGAAGATGACGTG [11111111111111111111111111111111111	Qy 13/1 CTGGATCTTGAAATAGAGTTGCACTTGCTCAACGTCTTTTCAACGGAACCACAACT 1430	DD 1381 GCAATGGCGAAATGAAGGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCT 1440 QY 1491 GACCGTCTCACTGGTACGAACATCACGGGGTGTAAAGATAGCACTTTCAGAATC 1550 QY 1441 CACCGTCTACACAACAACAACAACAACAACAACAACAACAACAAC	1551 CTAGAAGAGCATCAAAAGTAGACTAAAAGCGCTTTCTAAAACCGTGGAACTCGGGAAACGA 1551 CTAGAAGAGCATCAAAAGCGCTTTCTAAAACCGTGGAACCA 11111111111111111111111111111111	1611 TPCTTCCCGCGCTGTTCGGCAGTGCTCGACCAGATTATCAACTGTGAGGACTTGACTCAA	1671 CTGGCTTGCGGAGAAGACGACTGCTGAGAAACGACTACAAAAGAAGGAAG	1731 GAANTACAAGAGACATTAAGAAGGCCITTAGTGAGAAATTTGGAATTAGGAATTGG 	1791 TCCTGACAGATTCGACTTCTTCCACATCGAAATCAACCGGTGGAAAGAGGTCTAACCGT			1971 CGCTCTTCGTTTTGCATCCTGTGTATTATTGC 1921 CGCTCTTCGTTTTGCATCCTGTGTATTATTGCATCTGTGTATTGTATTGCATCTGTGTATGTATGTA	Oy 2031 ACANTTGAACCANTGGRATTGTA 2061 Db 1981 ACANTTGAACCAATGGTATACAGATTGTA 2011	RESULT 4 AAV43661 ID AAV43661 standard; cDNA; 2011 BP.	AC AAV43661; XX DT 29-SEP-1998 (first entry)
Matches 2008; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Qy 51 GATCTCTTTAATTGTGAATTCAATTCAACGGAACCTGTTGATGGACACCATTGAT 110 Db 1 GATCTCTTTAATTTGTGAATTTCATCGGAACCTGTTGATGGACCACCATTGAT 60 Qy 111 GGATCGCGATTCTTAATTTTATGAATTCATCGCAACCTTTTTCATCGCAACCTTTAATTGATGAATCATCGCAACCTTTTTAATTTTAATTCTTTAATTTAATTTTAATTTTAATTTTAATTTAATTTTAATTTT	Db 61 GGATTGGCGATTGTTATGAAATCAGCACTAGTTTCGTCGCTACCGATAACACCGAC 120 Qy 171 TCCTCTATTGTTATCTGGCGCGAAGAAGTACTCACCGGACCTGATGTATCTGCTCTG 230	QY 231 CAATTGCTCTCCAACAGCTTCGAATCCGTCTTTGACTCGCGGATGATTTCTACAGCGAC 290	Qy 291 GCTAAGCTTGTTCTCTCCGACGGCCGGGAAGTTTCTTTCCACCGGTGCGTTTTGTCAGCG 350 	OY 351 AGAAGCTCTTTCTTCAAGAGCGCTTTAGCCGCCGCTAAGAAGGAGAAAGACTCCAACAAC 410	Db 361 ACCGCCGCGTGAAGCTCGAGCTTAAGGAGATTACCAAGGATTACGAAGTTCGAT 420 Qy 471 TCGGTTGTGACTGTTTTGGCTTATGTTTACAGCAGGAGGAGGAGGACGCGCCGCCTTAAAGGA 530 LILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	531 GTTTCTGAATGCCCAGACGAGAATTGCTGCCACGTGCCTTGCCTGCC	Qy 591 AFGTTGGAGGTTCTCTATTTGGCTTTCAAGATCCCTGAATTAATT	Qy 651 CAGAGGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTATACTC 710	AAGCTTGCTAATATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGATGTAAAGAGATT	OY 771 ATTGTCAAGTCTAATGTAGATATGGTTAGTCTTGAAAAGTCATTGCCGGAAGAGGTTGTT 830	AAAGAGATAATTGATAGACGTAAAGAGCTTGGTTTGGAGGTACCTAAAGTAAAGAACAT 	891 GTCTCGAATGTACATAAGGCACTTGACTCGGATGATTGAGTTAGTCAAGTTGCTTTTG 	Qy 951 AAAGAGGAFCACCAATCTAGAFGAFGAGGTGTGCTTTCATTTCGCTGTTGCATAFTGC 1010 	OY 1011 AATGTGAAGCGGCAACAGATCTTTAAAACTTGACGATGTCAACCATAGGAAT 1070 	Qy 1071 CCGAGGGGATATACGGTGCTTCATGTTGCTGCGAAGGAGCCACAATTGATACTA 1130

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P-PSDB; AAW61983
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27-DEC-1996,
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                                           8-JUN-1998
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                                                                        Uknes SJ;
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                          mutation
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AATGTGAAGACCGCAACAGATCTTTAAAACTTGATCTTGCCGATGTCAACCATAGGAAT 1070
         Sequence 2011 BP; 563 A; 417 C; 474 G; 557 T; 0 other;
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                                                          Query Match
Best Local Similarity 99.9%;
Matches 2008; Conservative
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inducible immunity-1 (NIM1) protein. Sequences shown in AAV43661 to
AAV43665 represent variants of the NIM1 cDNA. The invention provides a
chimeric gene comprising a promoter active in plants operatively linked
co a DNA molecule that encodes an altered form of the NIM1 protein. Plant
cells stably transformed with a recombinant vector comprising such a
chimeric gene have a broad spectrum of disease resistance. The altered
conting transformed with a netered NIM1 gene exhibits constitutive SAR
copured resistance (SAR) signal transduction pathway. The transgenic
companies transformed with an altered NIM1 gene exhibits constitutive SAR
capteression which is higher in the transformed plants than in a wild type
plant. The products can be used for producing plants with a broad
companies are resistance. Overapression of NIM1 mimics the effects
cof inducer compounds that induce constitutive immunity (CIM) phenotype
cof in plants. The inventions can be used with plants such as rice, wheat,
cof corr, potato, carrot, sweet potato, sugar beet, bean, pea,
chicory, lettuce, cabbage, cauliflower, broccoli, turnip, radish,
construction, aparico, sapplant, pepper, celery, carrot,
squash, pumpkin, zucchini, cucumber, apple, pear, quince, mango, banana, soybean, tobacco,
cherry, placapple, avocado, papaya, mango, banana, soybean, tobacco,
contacto, sorghum and sugarcane. The plants produced are resistant to
copiant pathogens such as viruses, viroids, fungi, bacteria, insects such
as aphids and lepidoptera and nematodes. The plants produced can be used
in agriculture.
                                                                 Non-inducible immunity-1 gene; NIM1 gene; disease resistance; mutant; transgenic plant; SAR; systemic acquired resistance; CIM; pathogen; constitutive immunity; agriculture; variant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of non-inducible immunity-1 gene - for transforming plants to produce transgenic plants having a broad spectrum disease resistance
                        Non-inducible immunity-1 (NIM1) protein variant 1 encoding cDNA
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/note= "wild type TGC is replaced by GCC"
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/note= "wild type TCG is replaced by GCG"
                                                                                                                                                                                                                                                                                                   "NIM1 protein variant 1"
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96US-0033177.
96US-0034379.
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                                                                                                                                                             Arabidopsis thaliana.
Synthetic.
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                                                                                                                                                                           GCTAAGCTTGTTCTCTCCGACGGCCGGGAAGTTTCTTTCCACCGGTGCGTTTTGTCAGCG
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                                                                                                                        ACCGCCGCCGTGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGAT
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                                                                   171 TCCTCTATTGTTTATCTGGCCGCCGAACAAGTACTCACCGGACCTGATGTATCTGCTCTG
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 Length
  DB 19;
Score 2006.2;
Pred. No. 0;
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CAACCATAGGAAT	PTGATA 	ACCGCP 1 1 1 1	AATGC	GAGAA 	ATGACGCTG	SCACAA SCACAA	TCGAG	TCAGA	GGAAA GGAAA	TGACT	GGTAC	GAAAT 	CTAACCGT	GCTGTACCAT	CATATAGTTT 	ATGTT 	
GTCAAC	CACAA? CACAA?	GTAGA/ GTAGA/	CGGAGG CGGAGG	ACAAAC ACAAAC	TGAAG TGAAG	CGGAAC	CTAGC CTAGC	CACCET	AACTCC AACTCC	AGGACT AGGACT	AGCAAA AGCAAA	AATTAC	AGAGGT AGAGGT	TTTGC	SCGTCA	AAACAA AAACAA	
CGATG	AGGAGC AGGAGC	GGAAG 	TATCC TATCC	AGAAG AGAAG	TGAAT 	TCCAA TCCAA	AGTGA 	GATAG	CGTGG	CTGTG,	AAAGAJ AAAGAJ	TTTGG	TGGAA TGGAA	GTAAT: GTAAT:	rcgrrggcgrc 	GTGCTTCAAACAAATGTTC 	
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ybridisation assay; genetic mapping; gene expression control; rotein identification; signal transduction pathway; etabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                          rabidopsis thaliana DNA fragment SEQ ID NO: 18587.
AC37765 standard; DNA; 2024 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This genomic DNA sequence encodes the NIM-1 protein from Arabidopsis thallana. This protein is used in a method resulting in the protection of an immunomodulated plant having a first level of resistance and involves treatment with at least 1 microbicide that confers a second level of resistance, such that the plants have a third level of resistance greater than the sum of the first two levels. The method can be applied to a wide variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect against viruses, fungl, bacteria, insects and nematodes. The method of microbicide used. Since the process involves two different methods of protection, it is unlikely that the pathogen will develop resistance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protection of immunomodulated plants against pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               applying microbicide to provide increase in resistance
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Pred. No. 0;
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Best Local Similarity 87.5%;
Matches 2088; Conservative
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96US-0034378
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                          CGAGAACAAATTCCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAATTGAAG
                                                                                             4195 AATTAAATTTATGTCCTCTCTATTAGGAAACTGAGTGAACTAATGATAACTATTCTTTGT
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Non-inducible immunity-1 gene; NIM1 gene; disease resistance; mutant; transgenic plant; SAR; systemic acquired resistance; CIM; pathogen; constitutive immunity; agriculture; ss.
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                                                     A. thaliana non-inducible immunity-1 (NIM1) protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                    "this is indicated as TGG in a different
part of the specification"
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/product= "wild-type NIM1
/note= "contains introns"
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                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lawton KA,
       ВР
       DNA; 5655
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96US-0033177.
96US-0034379.
96US-0034382.
97US-0034730.
97US-0035021.
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       standard;
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Uknes SJ;
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This DNA encodes the Arabidopsis thathan non-inductuble immunity in wild-type protein. This DNA can be mutated to produce altered forms of the NIMM protein. The invention provides a chimeric gene comprising a promoter active in plants operatively linked to a DNA molecule that encodes an altered form of the NIMM protein. Plant cells stably transformed with a recombinant vector comprising such a chimeric gene have a broad spectrum of disease resistance. The altered NIMM proteins act as dominant-negative regulators of the systemic acquired resistance (SAR) signal atransduction pathway. The transgenic plants transformed with a natered NIMI gene exhibits constitutive SAR expression which is higher in the transformed plants with a broad spectrum disease resistance. Overexpression of NIMI mimics the effects of inducer compounds that induce constitutive immunity (CIM) phenotype in plants. The inventions can be used with plants such as rice, wheat, barley, rye, corn, potato, carrot, sweet potato, sugar beet, bean, pea, chicory, lettuce, cabbage, cauliflower, broccoli, turnip, radish, spinach, asparagus, onion, garlic, apple, pear, quince, melon, plum, cherry, peach, nectarine, apricot, strawberry, grape, raspberry, blackberry, pineapple, avocado, papaya, mango, banana, soybean, tobacco, tomato, sorghum and sugarcane. The plants produced can be used in agriculture. the Arabidopsis thaliana non-inducible immunity-1 (NIM1)

Sequence 5655 BP; 1758 A; 1014 C; 1069 G; 1814 T; 0 other;

3; 3054 CTGTTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCCGCCTAAAGGAGTTTCTGAAT 3234 540 240 649 TCTTCAAGAGCGCTTTAGCCGCCGCTAAGAAGGAGAAAGACTCCAACAACACCGCCGCCG 420 CCAACAGCTICGAATCCGTCTTTGACTCGCCGGATGATTTCTACAGCGACGCTAAGCTTG 300 ATTIGIGAATTICAATICATCGGAACCIGITGATGGACACCACCATIGATGGATTCGCCG 120 1 TCGATCTTTAACCAAATCCAGTTGATAAGGTCTCTTCGTTGATTAGCAGAGATCTCTTTA 60 Indels 298; Gaps TGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTCGGTTGTGA CIGITITGGCTTATGTTTACAGCAGCAGAGTGAGACCGCCGCCTAAAGGAGTTTCTGAAT TICICICGACGGCCGGGAAGITICITICCACCGGTGCGTTTTGTCAGCGAGAAGCTCTT TTTATCTGGCCGCCGAACAAGTACTCACCGGACCTGATGTATCTGCTCTGCAATTGCTCT Length 5655; 601 TICTCTATTIGGCTTTCATCTTCAAGATCCCTGAATTAATTACTCTCTA---0; DB 19; Score 1760; DB Pred. No. 0; Mismatches 83.78; 87.58; Best Local Similarity 87.5 Matches 2088; Conservative Query Match 2995 3175 3235 3055 3115 61 2755 181 241 301 361 421 481 a ò g ò g ò g ò qq ò q ò οg ò q ŏ qq ô g ò

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Qy	. 059	64	
qq	2	CCATCTGCATTAAGCTATGGTTACACATTCATGAATATGTTCTTACTTGAGTACTTGTA 34	4
Qy	650	TCAGAGGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTG 70	0
q	15	TCAGAGGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTG 34	4 1
VQ 4G	702 0	GGAGCTATIGGATAGAIGT 76 	
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qq	3595 (CTTGTTAAAGAGATAATTGATAGACGTAAAGAGCTTTGGTTTTGGAGGTACCTAAAGTA 36	9
ολ	882	AATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAG 94	
qq	3655	SAAACATGTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAG 3/	_
Qy D	942	ATCTAGATGATGCGTGTGCTCTTCATTTCGCTGTT 10 	
ò	002	CATATTGCAATGTGAAGACCGCAACAGATCTTTAAAACTTGATCTTGCCGATGTCAAC 10	90
g qq	75		83
Οy	1062	GATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAA 11	12
qa	3835	ATAGGAATCCGAGGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAA 38	83
Ολ	122	TIGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGA 11	18
qq	92	SATACTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGA 39	י תכ
Qy	182	CATGATCGCAAAACCAGCCACTATGGCGGTTGAATGTAATATATCCCGGAG 12	
qq	3955	ogcactcatgatcgcaaaacaagccactatggcggttgaatgtaatatatcccggag 40	-
Qy	1242	ATGTGTAGAAATACTAGAGCAAGAAGACAAA 1	30
3 8	300	aanaaammoomagamgmmoomoomoomagagagagagagagag	1361
OP OP	4075	CTAGAGATGTTCCTCCCTCTTTTCCAGTGCGCCGCTGATGAATTGAAG 4	13
QY		GACGCTGCTCGATCTTGAAAATAG1	38
qq	4135		19
ΟY	1388	1	38
qq	4195	IAAATTTATGTCCTCTCTATTAGGAAACTGAGTGAACTAATGATAACTATTCTTTGT 4	25
Qy	1388	AGTIGCACTIGCTCAACGICTTTTCCAACGGAAGCACAAGCIGCA 1	1433
ò	4255	3TCCACTGTTTAGTTGCACTTGCTCACGTCTTTTTCCAAGGGAAGCAAAGCTGCA 4	31
δy		CCGAAATGAAGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCTGAC 1	49
QQ	4315	<pre>GGAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCTGAC</pre>	י רי
δy	1494	CGTCTCACTGGTACGAAGAAGAACATCACCGGGTGTAAAGATAGCACCTTTCAGAATCCTA 15	52

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4375 CGTCTCACTGGTACGAAGAGAACATCACCGGGTGTAAAGATAGCACCTTTCAGAATCCTA 4434
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                                                                                                        GAAGACGACACTGCTGAGAAACGACTACAAAAGAAGCAAAGGTACATGGAAATACAAGAG 1742
                                                                                                               1743 ACACTAAAGGAGCCTTTAGTGAGGACAATTTGGAATTAGGAAATTCGTCCCTGACAGAT 1802
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                                                                                                                                                             CGTCGTCGGTGAGACTCTTGCCTCTTAGTGTAATTTTTGCTGTACCATATAATTCTGTTT 1922
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                                                          1623 IGTTCGGCAGTGCTCGACCAGATTATGAACTGTGAGGACTTGACTCAACTGGCTTGCGGA
                                                                                        4615 TGTTCGGCAGTGCTCGACCAGATTATGAACTGTGAGGACTTGACTCAACTGGCTTGCGGA
                  4495 CATCGGACTCCTTATCACAAAAAACAAAACTAAATGATCTTTAAACATGGTTTTGTTACT
                                                                                                                                                       TCGACTTCTTCCACATCGAAATCAACCGGTGGAAAGAGGTCTAACCGTAAACTCTCTCAT
                                                                                                                                                                                                                                   2043 AATGGTATACAGATTTGTAATATATTTTATGTACATCAACAATAA 2088
                                                                                                                                                                                                                                                           noninducible immunity; disease resistance; plants;
            GAAGAGCATCAAAGTAGACTAAAAGCGCTTTCTAAAACC-
                                                                                                                                                                                                                                                                                                                                                                                        /product= "NIM1 protein"
2787.3347
                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana NIM1 gene.
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/*tag= a
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4271..4474
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3427..4162
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                                                                                                                                                                                                                                                                                                                                                  gene expression; ss
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                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                            NIM1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence is that of the NIM1 (noninducible immunity) gene. It may be used to confer a broad spectrum disease resistance in plants, specifically crop plants, e.g. rice, wheat, barley, rye and corn. The NIM1 gene can be used to confer universal disease susceptibility to plant cells, and their progeny. It can also be used in a screening method for identifying compounds capable of inducing broad spectrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2695 TCGATCTTTAACCAAATCCAGTTGATAAGGTCTCTTCGTTGATTAGCAGAGAGTCTCTTTA 2754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIM1 gene which allows activation in plant of systemic acquired resistance - useful to confer broad spectrum disease resistance in plants, specifically crop plants, e.g. rice, wheat, barley, rye and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease resistance in plants, while the plant cells, and their progeny, can be used to isolate a gene fragment which allows expression of broad spectrum disease resistance in plants, or to incorporate the resistant trait into plant lines through breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TCGAICTTTAACCAAATCCAGTTGATAAGGTCTTTCGTTGATTAGCAGAGATCTCTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Friedrich LB,
Weymann K;
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96us-0020272.
96us-0024883.
96us-0033177.
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Matches 2088; Conserv
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30-AUG-1996;
13-DEC-1996;
27-DEC-1996;
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οy	361	CTTCAAGAGGGGTTTAGCCGCCGCTAAGAAGAGAAAAACACTCCAACAACACGCCGCCG 42	0
Dp	3055		
Oy Db	421	TGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTCGTTGTGA 48(0 74
λο d	481	CIGITITGGCTTAIGITIACAGCAGAGAGGGACCGCCGCCCTAAAGGAGTTICIGAAI 54(0 34
λŏ	54	SCAGACGAGAATTGCTGCCACGTGGCTTGCCGGCCGGCGGTGGATTTCATGTTGGAGG 60	0
Db	3235	GCGCAGACGAGAATTGCTGCCACGTGGCTTGCCGGCCGGC	94
yo g	3295	TICICIATITGGCTITCAICTICAAGAICCCIGAATTAATTACICICIA 64(54
λ̈́o	65		
g	3355	ACCATCTGCATTAAGCTATGGTTACACATTCATGAATATGTTCTTACTTGAGTACTTGTA 34	14
οy	650	TCAGAGGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTG 70	г
qo	3415	TTTGTATTTCAGAGGCACTTATTGGACGTTGTTAGACAAAGTTGTTATAGAGGACACATTG 34	74
Qy Dp	702 3475	GTTATACTCAAGCTTGCTAATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGATGT 76	.1 .34
à	3535	AAAGAGATTATTGTCAAGTCTAATGTAGATATGGTTAGTCTTGAAAAGTCATTGCCGGAA 82 	11
ò	82	GAGCTTGTTAAAGAGATAATTGATAGACGTAAAGAGCTTGGTTTGGAGGTACCTAAAGTA 88	
g qq	6		54
oy B	882	AAGAAACATGTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAG 94	.1 .14
ογ	94	TTGCTTTGAAAGAGATCACACCAATCTAGATGATGCGTGTGCTTTTCGCTGTT 1	101
Op	3715	TTGCTTTTGAAAGAGGATCACACCAATCTAGATGATGCGTGTGCTCTTCATTTCGCTGT	74
ŏ	8 6	GCATATTGCAATGTGAAGACGCAACAGATCTTTAAAACTTGATCTTGCCGATGTCAAC 1	(a)
a	_	GCATATTGCAATGTGAAGACCGCAACAGATCTTTAAAACTTGATCTTGCCGATGTCAAC	າ 1
Oy Dp	1062 3835	CATAGGAATCCGAGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAA 11	121 394
οy	1122	E+ -	181
qq	3895		154
οy	1182	-	241
QQ	3955	- «	114
ογ	24	CAATGCAAGCATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGAAGAAA 1	0 1
QQ	4015	CAATGCAAGCATTCTCTCTAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAAAAA 4	_
Oy Db	1302	CGAGAACAAATTCCTAGAGATGTTCCTCCCTCTTTTGCAGTGGCGGCGGCGATGAATTGAAG 1. 	361 134

Οy	62	SACGCTGCTCGATCTT	138/
Dp	135		4194
Qy	1388		1387
QQ	4195	FAAATTTATGTCCTCTCTATTAGGAAACTGAGTGAACTAATGATAACTATTGT	4254
Qy	88	AGTTGCACTTGCTCACGTCTTTTCCAACGGAAGCACAAGCTGCA	43
Dp	4255	TGTTTAGTTGCACTTGCTCAACGTCTTTTTCCAACGGAAGCACAAGCTGCA	-i
QY	434	ATGGAGATCGCCGAAATGAAGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCTGAC	49.
qq	315	SAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTGACTTGAGCCTCGAGCCTGAAC	ט ר
δ.	9 1	GAATCCTA 	n m
90 20	1554	CCCTGGTACGAAGAACAACATCACCGGGGTGTAAAAGATAGCCCCTTTCAGAACTACCTA	59.
g 8	435	ACCCACTT	
δy	1593		1592
qq	4495	CGGACTCCTTATCACAAAAACAAAACTAAATGATCTT	
δy	1593	GTGGAACTCGGGAAACGATTCTTCCGGGC	C)
QQ	4555	ACGATTCTTCCCG	4614
Qy	1623		.89
qq	4615	GTTCGGCAGTGCTC	4674
δŏ	683	GAAGACGACTGCTGAGAAACGACTACAAAAGAAGCAAGGTACATGGAAATACAAGAG 	1742
o c	0 5	AGARACGACI ACRARAGORAGO CARAGOI ACOI GORANI E E EL CONTROL DE CARA CONTROL DE	
g G	4735	ACACTAAAGAAGGCCTTTAGTGGGGGACATTTGGGATTAGGGAAATTGCGCCTGACGGT 	6,
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S q	79	TCGACTTCTTCCACATCGAAATCAACCGGTGGAAAGAGGTCTAACGGTAAACTCTCTCAT	æ
δy	1863	STCGTCGGTGAGACT	1922
qq	4855	3AGACTCTTGCCTCTTAGTGTAATTTTTGCTGTACCATATAATT	4914
δŽ	1923	TCATGATGACTGTAACTGTTTATGTCTATCGTTGGCGTCATATAGTTTCGCTCTTTCGTTT	1982
QQ	4915	CATGATGACTGTATCTTTATGTCTATCGTTGGCGTCATATAGTTTCGCTCTTCGTT	4974
Qγ	1983	TGCATCCTGTGTATTATTGCTGCAGGTGTGCTTCAAACAAA	Ó
QQ	4975	GCATCCTGTGTATTATTGCTGCAGGTGTGCTTCAAACAATGTTGTAACAATTTGAAC	5034
οy	2043	AATGGTATACAGATTTGTAATATATATTTATGTACATCAACAATAA 2088	
QQ	5035	ggtatacagatttgtaatatatatttatgtacatcaacaat	
m ~	ULT 9 43658/c	٠	
0 X	AV4	658 standard;	
Y X	AAV4	3658;	
E X	29-SI	EP-1998 (first entry)	

us-08-908-884-2.rng

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This represents the genomic sequence of the Arabidopsis thaliana noninducible immunity-1 (NIM1) gene. The invention provides a chimeric gene comprising a promoter active in plants operatively linked to a DNA molecule that encodes an altered form of the NIM1 protein. Plant cells stably transformed with a recombinant vector comprising such a chimeric gene have a broad spectrum of disease resistance. The altered NIM1 comparison act as dominant-negative regulators of the systemic acquired resistance (SAR) signal transduction pathway. The transgenic plants fransformed with an altered NIM1 gene exhibits constitutive SAR cexpression which is higher in the transformed plants than in a wild-type plant. The products can be used for producing plants with a broad spectrum disease resistance. Overexpression of NIM1 mimics the effects of inducer compounds that induce constitutive immunits with a broad confined compounds that induce constitutive immunity (IMP) phenotype in plants. The inventions can be used with plants such as e.g. rice, wheat, callory, lettuce, cabbage, calliflower, broccoli, turnip, radish, spinach, asparagus, onlon, gazilic, egyplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, quince, melon, plum, certerny, pacah, nectarine, aprincot, strawberry, grape, rasperry, corn, postab, nectarine, aprincot, strawberry, grape, rasperry, corn, plants, aviroids, fundi, bacteria, insects such as viruses, wincids, fundi, pateria, and lear domardor mandon pateria, and nematods mandon pateria, and nematods mandon pateria, and nematods mandon pateria, and lear domardor mandon pateria, and lear
                                            Non-inducible immunity-1 gene; NIM1 gene; disease resistance; mutant; transgenic plant; SAR; systemic acquired resistance; CIM; pathogen; constitutive immunity; agriculture; ss.
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thaliana non-inducible immunity-1 (NIM1) genomic sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ryals JA,
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96US-0033177.
96US-0034382.
97US-0034730.
97US-0035021.
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                                                                                                                                            Arabidopsis thaliana
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Ġ. Gaps Indels 298; DB 19; Length 9919; Sequence 9919 BP; 3150 A; 1825 C; 1737 G; 3207 T; 0 other; ; 0 Score 1760; DB Pred. No. 0; 0; Mismatches Query Match 83.7%; Best Local Similarity 87.5%; Matches 2088; Conservative

nematodes. The plants produced can be used

.....yens such as viruses, aphids and lepidoptera and agriculture.

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3807 61 g QΥ

1122 TTGATACTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGA 1181

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3207 ACCATCTGCATTAAGCTATGGTTACACATTCATGAATATGTTCTTACTTGAGTACTTGTA 3148 3147 TTTGTATTCAGAGGCACTTATTGGACGTGTTGTAGAGGACACATTG 3088 TIGCTTTTGAAAGAGATCACACCAATCTAGATGATGAGGGTGTGCTCTTCATTTCGCTGTT 1001 761 ATTCTTATGAAATCAGCAGCACTAGTTTCGTCGCTACCGATAACACCGACTCCTCTATTG TTTATCTGGCCGCCGAACAAGTACTCACCGGACCTGATGTATCTGCTCTGCAATTGCTCT CCAACAGCTTCGAATCCGTCTTTGACTCGCCGGATGATTTCTACAGCGACGCTAAGCTTG TGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTCGGTTGTGA GAGCTTGTTAAAGAGATAATTGATAGACGTAAAGAGCTTGGTTTGGAGGTACCTAAAGTA TCTTCAAGAGGGCTTTAGCCGCCGCTAAGAAGGAGAAAGACTCCAACAACACCGCCGCCG CTGTTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCCGCCTAAAGGAGTTTCTGAAT -----TCAGAGGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGACACATTG AAAGAGATTATTGTCAAGTCTAATGTAGATATGGTTAGTCTTGAAAAGTCATTGCCGGAA TTGCTTTTGAAAGAGGATCACACCAATCTAGATGCGTGTGTGCTCTTCATTTCGCTGTT GTTATACTCAAGCTTGCTAATATATGTGTGAAAGCTTGTATGAAGCTATTGGATAGATGT **AAGAAACATGTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAG** GCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAAACTTGATCTTGCCGATGTCAAC CATAGGAATCCGAGGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAA 3747 3687 3627 3507 3447 3327 3267 3087 2967 2907 2847 1002 2787 1062 181 301 3567 421 481 3387 541 601 650 702 762 3027 822 882 241 361 942 qq δλ qq qq qq qq qq qq pp Q δ δ δλ δy δy qq δλ q g pp δy Dp Dp Q qq qq q ŏ QΥ Qγ δŻ q Qy ΩŸ οy οy

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CGAGAACAAATTCCTAGAGATGTTCCTCCCTCTTTTGCAGTGGCGGCCGATGAATTGAAG
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                      ACCGCACTCATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATATCCCGGAG
                                                              ATGACGCTGCTCGATCTTGAAAATAGAGGTATCTATCAAGTCTTATATTTGTTTTG
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                                                                                                                                                                                                                                                                                  ---GTGGAACTCGGGAAACGATTCTTCCCGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIM1 gene which allows activation in plant of systemic acquired resistance - useful to confer broad spectrum disease resistance in plants, specifically crop plants, e.g. rice, wheat, barley, rye and
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                                                                                                                                                                                                                                                                                                                                                                                   NIM1; noninducible immunity; disease resistance; plants; SAR gene expression; ss.
                                                                 AATGGTATACAGATTTGTAATATATTTATGTACATCAACAATAA
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Conservative (
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121 ATTCTTATGAAATCAGCAGCACTAGTTTCGTCGCTACCGATAACACCGACTCCTCTATTG	181 TITAICTGGCCGCGAACAAGTACTCACCGGACCTGATGTATCTGCTCTGCAATTGCTCT 	241 CCAACAGCITCGAATCCGICTTIGACICGCCGGATGAITICTACAGCGACGCTAAGCTIG	301 TTCTCTCCGACGCCGGGAAGTTTCTTTCCACCGGTGCGTTTTGTCAGCGAGAAGCTCTT	361 TCTTCAACAGCGCTTTAGCCGCCGCTAAGAAGGAGAAAGACTCCAACAACACGCCGCGCGCG	421 TGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTCGGTTGTGA 	481 CTGTTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCCGCCTAAAGGGGTTTCTGAAT 	541 GCGCAGACGAGAATTGCTGCCACGTGGCTTGCCGGCCGGC	601 TICICTATITIGGCITICALCTICAAGATCCCTGAATTAATTACTCTCTA		3207 ACCATCTGCATTAAGCTATGGTTACACATTCATGAATATGTTCTTACTTGAGTACTTGTA	650TCAGAGGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTG 	702 GITAIACTCAACCTIGCTAATAIAIGTGGTAAAGCTIGIAIGAAGCTAITGGAIAGAIGT 	762 AAAGAGATTATTGTCAAGTCTAATGTAGATATGGTTAGTCTTGAAAAGTCATTGCCGGAA 	822 GAGCTTGTTAAAGAGATAATTGATAGACGTAAAGAGCTTGGTTTGGAGGTACCTAAAGTA 11111111111111111111111111111111	882 AAGAAACATGTCTCGAATGTACATAAGGCACTTGACTCGGATGATAGATA	942 TIGCTITIGAAAGAGGAICACACCAATCIAGAIGATGCGIGIGCGCTTTGATITICGCTGTT	1002 GCATATTGCCAATGTGAAGACCGCAACAAGATCTTTAAAACTTGATCTTGCCGATGTCAAC	1062 CATAGGAATCCGAGGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAA
Qy Db	Oy Dp	Qy Dp	Oy Db	QY Db	Qy Db	Qy Db	Oy Op	Qy Dp	δλ	QQ	Qy Db	QY Db	Qy Db	QY	oy ob	QY Db	Qy Db	Qy Db

Qy Db	1122	TTGATACTATCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGA 1 	1181
Oy 4		ACCGCACTCATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATATCCGGAG 1	C)
an .	9	CCGCACTCATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATATCCCGGAG	4
λο qa	1242	CAATGCAAGCATTCTCTCAAAGGCGGACTATGTGTAGAATTACTAGAGCAAGAGACAA 1 	1301
δò	0	GAGAACAAATTCCTAGAGATGTTCCTCCTTTTTGCAGTGGCGGCCGATGAATTGAAG	, ,
qq	4	CCGATGAATTGAAG	42
Qy	1362	3ACGCTGCTCGATCTTGAAAATAG	1387
qq	2427		2368
QY	1388		1387
qq	2367	TTAAATTTATGTCCTCTCTATTAGGAAACTGAGTGAACTAATGATAACTATTCTTTGT	2308
QY	1388	TTTTTCCAACGGAAGCACAAGCTGCA	1433
DÞ	2307	ACTGTTTAGTTGCACTTGCTCAACGTCTTTTTCCAACGGAAGCACAAGCTGCA	2248
Qy	43	AIGGAGAICGCCGAAAIGAAGGAACAIGIGAGTICAIAGIGACTAGCCTCGAGCCTGAC 1	1493
QQ	2247	GGAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCTGAC	2188
oy d	1494	CTTTCAGAATCCTA	55
3	٩	GICICACIGGIACGAAGAAGAICACCGGGIGIAAAGAIAGCACCIITCAGAAICCIA	2128
yo da	1554	E	59
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q q	2067	ATCGGACTCCTTATCACAAAAACAAAACTAAATGATCTTTAAACATGGTTTTGTTACT	2008
Qy	1593		1622
qq	2007	TTGTTTTTTTTATCATCAGTGGAACTCGGGAAACGATTCTTCCCGCG	94
QY	1623	SACCAGATTATGAACTGTGAGGACTTGACTCAACTGGCTTGCGG	68
QQ	1947	GTTCGGCAGTGCTCGACCAGATTATGAACTGTGAGGACTTGACTCAACTGGCTTGCGGA	88
Qy	1683	GAAGACGACACTGCTGAGAAACGACTACAAAAGAAGCAAAGGTACATGGAAATACAAGAG 1	1742
qq	1887	AAGACGACACTGCTGAGAAACGACTACAAAAGAAGCAAAGGTACATGGAAATACAAGA	82
Qy	1743	CAATTGGAATTAGGAAATTCGTCCCTGACAGA	80
οp	1827	CACTAAAGAAGGCCTTTAGTGAGGACAATTTGGAATTA	1768
Qγ	1803	GAAAGAGGTCTAACCGTAAACTCTCTCA	1862
QQ	1767	CGACTTCTTCCACATCGAAATCAACCGGTGG	70
Qy	1863	3CCTCTTAGTGTAATTTTTGCTGTACCATATAATTCTGTT	1922
Op	1707	GTCGTCGGTGAGCTCTTGCTTTAGTGTAATTT	1648
ΟY	1923	TTATGTCTATCGTTGGCGTCATATAGTTTCGCTCTTCGTTT 1	1982
QQ	1647	CATGATGACTGTAACTGTTTATGTCTATCGTTGGCGTCATATAGTTTCGCTCTTCGTTT 1:	
Qy	1983	IGCAICCTGIGIAITATIGCIGCAGGIGIGCITCAAACAAAIGTIGIAACAAITIGAACC 20	2042

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated plant acquired resistance polypeptide gene - useful for, e.g. producing plants with increased resistance to pathogens such as bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 19; Length 7548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is that of a 7.5 kb genomic region which contains the acquired resistance gene NPRI. The gene may be used in the production of transgenic cells which can produce the encoded acquired resistance protein. Such transgenic plants cells are useful in the production of plants having an increased level of resistance against disease caused by plant pathogens, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7548 BP; 2347 A; 1468 C; 1397 G; 2336 T; 0 other;
                                                                                                                                                                                                                                                                                                                                           gene; acquired resistance; disease; plant pathogens; plasma; fungi; insects; nematodes; viruses; viroids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nematodes, viruses,
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                                                                           AATGGTATACAGATTTGTAATATATATTTTATGTACATCAACAATAA
                                                                                                                                                                                                                                                                                                        thaliana 7.5kb region containing NPR1
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87.5%; Pred. No. 0;
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                                                                                                                                                                                         AAV16850 standard; DNA; 7548
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96US-0023851.
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Matches 2087; Conservative
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09-AUG-1996;
10-JAN-1997;
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              3361 ACCATCTGCATTAAGCTATGGTTACACATTCATGAATATGTTCTTACTTGAGTACTTGTA
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TTTATCTGGCCGCCGAACAAGTACTCACCGGACCTGATGTATCTGCTCTGCAATTGCTCT
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        1242 CAATGCAAGCATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGGAAGAAGAAAA
                                                                      CGAGAACAAATTCCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAATTGAAG
                                                                                                                                                                                                                       ATGGAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCTGAC
ACCGCACTCATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATATCCCGGAG
                                             4201 AATTAAATTTAIGTCCTCTCTATTAGGAAACTGAGTGAACTAATGATAACTATTCTTTGT
                                                                                                                                                                                    -------AGTTGCACTTGCTCAACGTCTTTTCCAACGGAAGCACGAAGCTGCA
                                                                                                                                                                                                                                                                                                                                                       4501 CATCGGACTCCTTATCACAAAAACAAACTAAATGATCTTTAAACATGGTTTTGTTACT
                                                                                                                                                                                                                                                                                                                                                                        ------GTGGAACTCGGGAAACGATTCTTCCCGCGCT
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This sequence encodes a truncated variant NIM-1 protein from Arabidopsis thaliana. This protein is used in a method resulting in the protection of an immunomodulated plant having a first level of resistance and involves treatment with at least 1 microbicide that confers a second level of resistance, such that the plants have a third level of resistance greater than the sum of the first two levels. The method can be applied to a wide variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect provides a high level of resistance and allows a reduction in the amount of micobicide used. Since the parhoses involves two different methods of protection, it is unlikely that the pathogen will develop resistance to
                                                                                                                                                                                                                                                                                                                                                                                                                        NIM-1; noninducible immunity; systemic acquired resistance; SAR; pathogen; disease; protection; immunomodulated; plant; cereal; fruit; vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protection of immunomodulated plants against pathogens applying microbicide to provide increase in resistance
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76.3%; Score 1605; DB 19;
100.0%; Pred. No. 0;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualiflers
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27-DEC-1996;
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                                                                                                                           wild-type
                       ATTCCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAATTGAAGATGACGCTG
                                                          CTCGATCTTGAAAATAGAGTTGCACTTGCTCAACGTCTTTTTCCAACGGAAGCACAAGCT
                                                                                            GCAATGGAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCT
                                                                                                                                                               CTAGAAGAGCATCAAAGTAGACTAAAAGCGCTTTCTAAAACCGTGGAACTCGGGAAACGA
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/note= "C-terminal deletion compared to
NIM1 sequence"
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96US-0033177.
96US-0034379.
96US-0034382.
97US-0035021.
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13-DEC-1996;
27-DEC-1996;
27-DEC-1996;
10-JAN-1997;
10-JAN-1997;
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AAV43663
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WPI; 1998-348536/30

Use of non-inducible immunity-1 gene - for transforming plants to produce transgenic plants having a broad spectrum disease resistance

Claim 12; Pages 155-159; 205pp; English.

This cDNA encodes an altered form of the Arabidopsis thaliana noninducible immunity-1 (NIMI) protein. Sequences shown in AAV43661 to
AAV43665 represent variants of the NIMI cDNA. The invention provides a
chimeric gene comprising a promoter active in plants operatively linked
to a DNA molecule that encodes an altered form of the NIMI protein. Plant
cells stably transformed with a recombinant vector comprising such a
chimeric gene have a broad spectrum of disease resistance. The altered
chimeric gene have a broad spectrum of disease resistance. The altered
continued session and altered NIMI gene exhibits constitutive SAR
appression which is higher in the transformed plants than in a wild-type
continued sease resistance. Overexpression of NIMI mimics the effects
cof inducer compounds that induce constitutive immunity (CIM) phenotype
cof inducer compounds that induce constitutive immunity (CIM) phenotype
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cof inducer compounds that induce constitutive immunity (CIM) phenotype
cof inducer compounds that induce of a garlic, sweet potato, sugar beet, bean, pea,
conforty, lettuce, cabbage, cauliflower, broccoli, turnip, radish,
conforty, pleach, nectarine, aprile, sweet potato, sugar beet, bear,
conforty, pleach, nectarine, aprile, symple, pear, quince,
cordunato, sorghum and sugarcane. The plants produced are resistant to
conforty plant pathogens such as viroids, fundi, bacteria, insects such
conforty in the pathogens and nematodes. The plants produced in agriculture.

Sequence 1608 BP; 447 A; 340 C; 385 G; 436 T; 0 other;

ó 410 61 GGATTCGCCGATTCTTATGAATCAGCAGCACTAGTTTCGTCGCTACCGATAACACCGAC 120 230 300 470 590 51 GATCTCTTTAATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACCACCATTGAT 110 121 TCCTCTATTGTTTATCTGGCCGCCGAACAAGTACTCACCGGACCTGATGTATCTGCTCTG 180 GCTAAGCTTGTTCTCTCCGACGGCCGGGAAGTTTCTTTCCACCGGTGCGTTTTGTCAGCG 350 Gaps AGAAGCTCTTTCTTCAAGAGCGCTTTAGCCGCCGCTAAGAAGAGGAGAAAGACTCCAACAAC TCGGTTGTGACTGTTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCCGCCTAAAGGA GGATTCGCCGATTCTTATGAAATCAGCAGCACTAGTTTCGTCGCTACCGATAACACCGAC TCCTCTATTGTTTATCTGGCCGCCGAACAAGTACTCACCGGACCTGATGTATCTGCTCTG CAATTGCTCTCCAACAGCTTCGAATCCGTCTTTGACTCGCCGGATGATTTCTACAGCGAC ACCGCCGCCGTGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGAT 0; Score 1605; DB 19; Length 1608; Pred. No. 0; Indels .; 0 Query Match 76.3%; Score 1605; D Best Local Similarity 100.0%; Pred. No. 0; Matches 1605; Conservative 0; Mismatches Query Match 111 231 241 171 181 291 351 301 411 361 471 421 531 g δλ a ŏ g g G Ω qq δλ qq ò g οy a à ò

1080 1430 1010 1250 AATGTGAAGACCGCAACAGATCTTTAAAACTTGATCTTGCCGATGTCAACCATAGGAAT 1070 950 900 096 770 720 830 780 710 GTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG 1081 TCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGAACCGCACTC ATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATATATCCCGGAGCAATGCAAG CATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGACAAACGAGAACAA ATTCCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAATTGAAGATGACGCTG 1261 ATTCCTAGAGATGTTCCTCCCTCTTTTGCAGTGGCGGCCGATGAATTGAAGATGACGCTG CAGAGGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTATACTC AAGCTTGCTAATATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGATGTAAAGAGATT AAAGAGATAATTGATAGACGTAAAGAGCTTTGGTTTGGAGGTACCTAAAGTAAAGAAACAT GTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG **AAAGAGGATCACACCAATCTAGATGATGCGTGTGCTCTTCATTTCGCTGTTGCATATTGC** AATGTGAAGACCGCAACAGATCTTTTAAAACTTGATCTTGCCGATGTCAACCATAGGAAT CCGAGGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAATTGATACTA TCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGAACCGCACTC CTCGATCTTGAAAATAGAGTTGCACTTGCTCAACGTCTTTTTCCAACGGAAGCACAAGCT GCAATGGAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCT GACCGTCTCACTGGTACGAAGAACATCACCGGGTGTAAAGATAGCACCTTTCAGAATC CTAGAAGAGCATCAAAGTAGACTAAAAGCGCTTTCTAAAAACCGTGGAACTCGGGAAAACGA ATTGTCAAGTCTAATGTAGATATGGTTAGTCTTGAAAAGTCATTGCCGGAAGAGCTTGTT INCITCCCGCGCTGTTCGGCAGTGCTCGACCAGATTATGAACTGT 1655 1561 601 831 781 891 841 901 1011 1071 1021 1131 1191 1141 1251 1201 1311 1371 1321 1431 1381 1491 1551 1501 1611 481 651 711 661 771 721 951 961 591 g g pp ōλ g QΥ g Dp QΥ qq δ g δ a δ pp qq Dp g QY g Dp ōλ g Ω qq ò QΫ́ Qγ δ QY Qγ Q QΥ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence encodes a truncated variant NIM-1 protein from Arabidopsis thaliana. This protein is used in a method resulting in the protection of an immunomodulated plant having a first level of resistance and involves treatment with at least 1 microbicide that confers a second level of resistance, such that the plants have a third level of resistance greater than the sum of the first two levels. The method can be applied to a wide variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect against viruses, fungi, bacteria, insects and nematodes. The method of micobicide used. Since the process involves two different method of micobicide used. Since the process involves two different methods of protection, it is unlikely that the pathogen will develop resistance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            582
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                                                                                                                            NIM-1; noninducible immunity; systemic acquired resistance; SAR; pathogen; disease; protection; immunomodulated; plant; cereal; fruit; vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Protection of immunomodulated plants against pathogens applying microbicide to provide increase in resistance
                                                                                                         A, thaliana N-terminal truncated NIM-1 variant cDNA #1.
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Pred. No. 0;
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/*tag= a
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/note= "variant"
                                             ВР
                                             AAV46276 standard; cDNA; 1597
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Best Local Similarity 99.9%;
Matches 1594; Conservative
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96US-0034378
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P-PSDB; W6447.
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                                                                                                                                                                                                                                      946 IITIGAAAGAGGATCACACCAATCTAGAIGATGCGTGTGCTCTTCAITTCGCTGTTGCAI
                                                                                                                                                                                                                                                                                TACTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGAACCG
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           TCTATCAGAGGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTA
                                                                                        TACTCAAGCTTGCTAATATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGATGTAAAG
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ATTCGTCCCTGACAGTTCGACTTCTTCCACATCGAAATCAACCGGTGGAAAGAGGTCTA 1845
                                                                                                                                                                                            ACCGTAAACTCTCTCATCGTCGTCGTGAGACTCTTGCCTCTTAGTGTAATTTTTGCTGT 1905
ACATGGAAATACAAGAGACACTAAAAGAAGGCCTTTAGTGAGGACAATTTGGAATTAGGAA 1785
                                                                                                                                                                                                                                                                                            Non-inducible immunity-1 gene, NIM1 gene; disease resistance; mutant; transgenic plant; SAR; systemic acquired resistance; CIM; pathogen; constitutive immunity; agriculture; variant; ss.
                                                                                                    1262 ACATGGAAATACAAGAGACACTAAAGAAGGCCTTTAGTGAGGACAATTTGGAATTAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCATATAATTCTGTTTTCATGATGACTGTAACTGTTTATGTCTATCGTTGGCGTCATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "NIM1 protein variant 2" /note= "N-terminal deletion compared to wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Non-inducible immunity-1 (NIM1) protein variant 2 encoding cDNA.
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV43662 standard; cDNA; 1597
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96US-0033177.
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P-PSDB; AAW61984.
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27-DEC-1996;
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This cDNA encodes an altered form of the Arabidopsis thaliana non-
inducible immunity-1 (NIM1) protein. Sequences shown in AAV43661 to

AAV44656 represent variants of the NIM1 cDNA. The invention provides a
chimeric gene comprising a promoter active in plants operatively linked
consistency stably transformed with a recombinant vector comprising such a
chimeric gene have a broad spectrum of disease resistance. The altered
chimeric gene have a broad spectrum of disease resistance. The altered
chimeric gene have a broad spectrum of disease resistance. The altered
consistence (SAR) signal transduction pathway. The transgenic
constraint and altered NIM1 gene exhibits constitutive SAR
expression which is higher in the transformed plants than in a wild-type
plant: The products can be used for producing plants with a broad
spectrum disease resistance. Overexpression of NIM1 mimics the effects
of inducer compounds that induce constitutive immunity (CIM) phenotype
cof inducer cambounds that induce constitutive immunity (CIM) phenotype
cof in plants. The inventions can be used with plants such as rice, wheat,
cof incory, lettuce, cabbage, cauliflower, broccoli, turnip, radish,
conticory, lettuce, cabbage, cauliflower, broccoli, turnip, radish,
conticory, peach, nectarine, aprailic, eggplant, pepper, celery,
conticory, pampkin, zucchini, cucumber, appare, peac, quince, melon, plum,
conterry, peach, nectarine, avocado, papaya, mango, banana, soybean, tobacco,
conterry, pathogens such as viruses, virioids, fundi, bacteria, insects such
contervants.
contervants produced are resistant to
contervants applies and nematodes. The plants produced can be used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 AAGGAGTTTCTGAATGCGCAGACGAGAATTGCTGCCGCGGCGGCGGCGGGGGG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         non-inducible immunity-1 gene - for transforming plants to
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Pred. No. 0;
0; Mismatches
                                                                          Claim 9; Pages 149-152; 205pp; English.
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99.9%;
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oy Ob	1006	ATTGCAATGTGAAGACGGCAACAGATCTTTAAAACTTGATCTTGCGGATGTCAACCATA 1065 	
oy D	1066	GGAATCCGAGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAATTGA 1125 	
çò Gp	1126	TACTATCTCTATTGGAAAAAGGTGCAACGGCATCAGAAGCAACTTTGGAAGGTAGAACCG 1185 	
Qy Dp	1186	CACTCATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATATCCCGGAGCAAT 1245 	
Qy Db	1246	GCAAGCATTCTCTCAAAGGCCGACTATGTGTAGAATACTAGAGCAAGAAGACAAAGGA 1305 	
Oy Dp	1306	AACAAATTCCTAGAGATGTTCCTCCCTCTTTGCAGTGGCGCCCGATGAATTGAAGATGA 1365 	
Oy Dp	1366 902	CGCTGCTCGAPCTTGAAAATAGAGTTGCACTTGCTCAACGTCTTTTCCAACGGAAGCAC 1425 	
Oy Dp	1426 962	AAGCTGCAATGGAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTGACTAGCCTCG 1485 	
Oy Db	1486	AGCCTGACCGTCTCACTGGTACGAAGAACATCACCGGGTGTAAAGATAGCACCTTTCA 1545 	
Oy Dp	1546	GAATCCTAGAAGAGCATCAAAGTACACTAAAAGCGCTTTCTAAAACCGTGGAACTCGGGA 1605 	
Qý Dp	1606	AACGATTCTTCCCGCGCTGTTCGGCAGTGCTCGACCAGATTATGAACTGTGAGGACTTGA 1665 	
Oý Dp	1666	CTCAACTGGCTTGCGGAGAAGACGACACTGCTGAGAAACGACAAAAGAAGAAAGGT 1725 	
Oy Dp	1726	acatggaaatacaagagacactaaagaaggcctttagtgaggacaatttggaattagga 1785 	
Oy Dp	1786	ATTCGFCCCTGACAGATTCGACTTCTTCCACATCGAAATCAACCGGTGGAAAGAGGTCTA 1845 	
Oy Db	1846	ACCGTAAACTCTCTCATCGTCGTCGGTGGGACTCTTGCCTCTTAGTGTAATTTTTGCTGT 1905	
Q.y	1906	ACCATATAATTCTGTTTTCATGATGACTGTATATGTCTATCGTTGGCGTCATAT 1965 	
Oy Dp	1966	AGTTTCGCTCTTCGTTTTGCATCCTGTGTATTATTGCTGCAGGTGTGCTTCAAACAAA	
Qy	2026	TTGTAACAATTTGAACCAATGGTATACAGATTTGTA 2061 	

Search completed: October 7, 2002, 22:58:29 Job time: 321.819 secs

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                                                                                                                                                       Description
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5: /cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Sequence 12, Appl Sequence 353, App Patent No. 5219739 Sequence 776, App Sequence 2, Applis Patent No. 5194596 Patent No. 5194199 Sequence 2, Applis Sequence 2, Applis Sequence 2, Applis Sequence 2, Applis Sequence 17, Applis	Sequence 11, Appl Sequence 13, Appl
US-08-545-196B-12 US-09-439-313-33 5219739-8 US-08-451-405A-2 5194596-8 5194596-16 5194596-16 5219739-16 US-09-385-982-494 US-09-385-982-427 US-08-353-700-2 US-08-353-700-2 US-08-353-700-2 US-08-153-700-2 US-08-100-2 US-08-100-2 US-08-100-2 US-08-100-2 US-08-100-2 US-08-100-2 US-08-100-2	US-08-487-826B-11 US-08-487-826B-13
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ALIGNMENTS

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APPLICANT: Uknes, Scott
APPLICANT: Whut, Michelle
APPLICANT: Steiner, Henry-York
APPLICANT: Ryals, John
TITLE OF INVENTION: ALTERED FORMS OF THE NIMI GENE CONFERRING
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAITIG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSE: No. 5986082artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 5986082th Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
APPLICATION NUMBER: US 60/035,021
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FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/989,478
                        Sequence 6, Application US/08989478
Patent No. 5986082
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
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US-08-989-478-6
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Sequence

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Conservative 0; Mismatches
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                                                                                                                                         LOCATION: 43.1824
OTHER INFORMATION: /product= "NIM1
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TELECOMMUNICATION INFORMATION:
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     TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                     LENGTH: 2011 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                   NAME/KEY: misc_feature
LOCATION: 1..2011
OTHER INFORMATION: /not
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Matches 2010; Conser
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                                                                   MOLECULE TYPE:
ORIGINAL SOURCE
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FEATURE
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1851 AAACTCTCTCATGGTCGTCGGTGAGACTCTTGCCTCTTAGTGTAATTTTTGCTGTACCAT 1910
                                                             ATAATTCTGTTTTCATGATGACTGTAACTGTTTATGTCTATCGTTGGCGTCATAGTTT 1970
                APPLICANT: Ryals, John
APPLICANT: Friedrich, Leslie
APPLICANT: Friedrich, Leslie
APPLICANT: Wolina, Antonio
APPLICANT: Wolina, Antonio
APPLICANT: Ruess, Wilhelm
APPLICANT: Knauf Beiter, Gertrude
APPLICANT: Knauf Ruth
APPLICANT: Kung, Ruth
APPLICANT: Costendorp, Michael
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. 6031153artis Corporation
                                                                                                                                                                                       ACAATTIGAACCAAIGGTATACAGATTIGIA 2061
                                                                                                                                                                                                        APPLICATION NUMBER: US 60/034,378
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
FILING DATE: 27-DEC-1996
PROR APPLICATION DATA:
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FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
APPLICATION NUMBER: US 60/035,024
FILING DATE: 10-JAN-1997
FILING DATE: 10-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/034,730 FILING DATE: 10-JAN-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/996,685
                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08996685 Patent No. 6031153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6031153th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                Patent No. 6031153
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
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PRILON AFFILICATION LAID.

APPLICATION NUMBER: US 08/875,015
FILING DATE: 16-JUL-1997
ATTONEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REPRENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1997 541-8689
INFORMATION EQ 199 541-8689
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 2011 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 1..2011
OTHER INFORMATION: /note= "NIM1 cDNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 43.1824
CTHER INFORMATION: /product= "NIM1 protein"
US-08-996-685-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 95.5%; Score 2009.4; Best Local Similarity 100.0%; Pred. No. 0; Matches 2010; Conservative 0; Mismatches
                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA ORIGINAL SOURCE: ORGANISM: Arabidopsis thaliana
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 Db	4 1 1	1801	1861	1921		RESULT 3 US-08-989-478-7 ; Sequence 7, Ap.	GENERAL INFOI APPLICANT: APPLICANT: APPLICANT:	APPLICANT TITLE OF TITLE OF	CORREST ADDRE STREE	STATE: STATE: COUNTR ZIP:	COMPOTER N MEDIUM T COMPUTER OPERATIN	CO		; APPLICAT ; APPLICAT ; FILING D ; PRIOR APPL	PF	PRIOR APPL APPLICAT FILING D		
651 CAGAGGCACTTATTGGACGTTGTAGAAGTTGTTATAGAGGACACATTGGTTATACTC 710 	711 AAGCTIGCTAATAITGIGGTAAAGCITGIAIGAAGCTATIGGAIAGAIGTAAGAGAIT 770 	771 ATTGTCAAGTCTAATGTAGATATGGTTAGTCTTGAAAAGTCATTGCCGGAAGAGCTTGTT 830 	831 AAAGAGATAATTGATAGAGGTAAAAGAGCTTGGTTTGGAGGTACCTAAAGTAAAGAAACAT 890 	891 GTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG 950 	951 AAAGAGGATCACCAATCTAGATGAGTGTGCTCTTCATTTGGCTGTTGCATATTGC 1010 	1011 AATGTGAAGACCGCAACAGATCTTTAAAACTTGATCTTGCCGATGTCAACCATAGGAAT 1070 	1071 CCGAGGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAGGGGCCACAATTGATACTA 1130 	1131 TCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGAACCGCACTC 1190 	1191 ATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATATTCCCGGAGCAATGCAAG 1250 	1251 CATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAGACAAACGAGAACGA 1310 	1311 AFFCCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAATTGAAGATGACGCTG 1370 	1371 CTCGATCTTGAAAATAGAGTTGCACTTGCTCAACGTCTTTTTCCAACGGAAGCACGAAGCT 1430 	1431 GCAATGGAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCT 1490 	1491 GACCGTCTCACTGGTACGAAGAGAACATCACCGGGTGTAAAGATAGCACCTTTCAGAATC 1550 	1551 CTAGAAGAGCATCAAAGTAGACTAAAAGGCCTTTCTAAAACCGTGGAACTCGGGAAACGA 1610 	1611 TTCTTCCCGCGCTGTTCGGCAGTGCTCGACCAGTTATGAACTGTGAGGACTTGACTCAA 1670 	1671 CTGGCTTGCGGAGAAGACCACTGCTGAGAAACGACTACAAAAGAAGGAAAGGTACATG 1730 	1731 GAAATACAAGAGACACTAAAGAGGCCTTTAGTGAGGACAATTTGGAATTAGGAAATTCG 1790
Oy Db	qa 1	Qy Dp	Oy Db	Qy Db	Qy Db	Qy Db	Oy Dp	Oy Dp	oy Op	Oy Dp	Qy Dp	Oy Dp	Oy Db	Qy	Qy	Qy Db	oy do	0y

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ITCTGTTTTCATGATGACTGTAACTGTTTATGTCTATCGTTGGCGTCATATAGTTT 1970
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                                                                                                                     CTCTCATCGTCGTCGTGAGACTCTTGCCTCTTAGTGTAATTTTTGCTGTACCAT 1910
                                                                                                                                       : Hunt, Michelle
: Steiner, Henry-York
: Ryals, John
INVENTION: ALTERED FORMS OF THE NIMI GENE CONFERRING
INVENTION: DISEASE RESISTANCE IN PLANTS
SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: Floppy disk
RR: IBM PC compatible
RN: SYSTEM: PC-DOS/MS-DOS
RE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
VION NUMBER: US/08/989,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCES: 32
IDENCE ADDRESS:
IEE: No. 5986082artis Corporation 3054 Cornwallis Road Research Triangle Park
No. 5986082th Carolina
                                                                                                                                                                                                                                                                                                                          TTTGAACCAATGGTATACAGATTTGTA 2061
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PPLICATION DATA:
CATION NUMBER: US 60/033,177
GDATE: 13-DEC-1996
CATION NUMBER: US 60/034,379
GDATE: 27-DEC-1996
GDATE: 27-DEC-1996
GDATE: 27-DEC-1996
GDATE: 27-DEC-1996
GDATE: 27-DEC-1996
GDATE: 17-DEC-1996
GDATE: 10-JAN-1997
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CATION NUMBER: US 60/035,022
G DATE: 10-JAN-11997
Y/AGENT INFORMATION:
Meigs, J. Timothy
RATION NUMBER: 38,241
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TION NUMBER: US 60/035,021
DATE: 10-JAN-1997
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986082
ORMATION:
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us-08-908-884-2.rni

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                AAAGAGGATCACCAATCTAGATGATGCGTGTGCTCTTCATTTCGCTGTTGCATATTGC
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     AAGCTTGCTAATATATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGATGTAAAGAGATT
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/note= "Serine residues at amino acid positions 55 and 59
wild-type NIM1 gene product have been changed to Alanine
residues."
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G's compared
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REPERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2011 base pairs
TYPE: nucleic acid
STRANEBUES: single
                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                 Score 2006.2;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                     /note= "nucleotides
changed from T's to
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                                                                                                                                                                                                                                                                                                 95.4%;
llarity 99.9%;
Conservative (
                                                                                                                                                                                                                               misc_feature
                                                                                                                                                       LOCATION: 43.,1824
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                          LOCATION: 205.217
OTHER INFORMATION:
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                                                                                                                                                                                           OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                     MOLECULE TYPE: CDNA FEATURE:
                                                                                                            linear
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2008; Conserv
                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                              NAME/KEY:
                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                   Query Match
Best Local Si
Matches 2008;
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                                                                                                                       1801 AAACTCTCTCATCGTCGTCGTGAGACTCTTGCCTCTTAGTGTAATTTTTGCTGTACCAT
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                                                                                        1851 AAACTCTCTCATCGTCGTCGGGGACTCTTGCCTCTTAGTGTAATTTTTGCTGTACCAT
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APPLICATION NUMBER: US/08/996,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Knauf-Beiter, Gertrude
APPLICANT: Knay, Ruth
APPLICANT: Kossmann, Helmut
APPLICANT: Oostendorp, Michael
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
CORRESPONDENCE: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6031153th Carolina CUUTRY: USA 21P: 7772
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
FILING APPLICATION DATA:
APPLICATION NUMBER: US 60/034,378
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
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FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
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Uknes, Scott
Molina, Antonio
Ruess, Wilhelm
Knauf-Beiter, Gertrude
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6031153
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COMPUTER READABLE FORM:
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APPLICANT:
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/product= "altered form of NIM1" /note= "Serine residues at amino acid positions 55 and 59 wild-type NIM1 gene product have been changed to Alanine residues."
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APPLICATION NUMBER: US 60/035,024 FILING DATE: 10-JAN-1997 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/875,015
                                                       FILING DATE: 16-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timochy
REGISTRATION NUMBER: 38,241
REPERENCE/DOCKET NUMBER: PF/5-
TELECOMMUNICATION INFORMATION:
TELEPRONE: (919) 541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2011 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 43..1824
OTHER INFORMATION: ,
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CHER INFORMATION:
CHER INFORMATION:
US-08-996-685-7
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OTHER INFORMATION:
FEATURE:
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Matches 2008; Conserv
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591 ATGTTGGAGGTTCTCTATTTGGCTTTCATCTTCAAGATCCCTGAATTAATT	651 CAGAGGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTATACTC [711 AAGCTTGCTAATATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGATGTAAAGAGATT 	771 ATTGTCAAGTCTAATGTAGATATGGTTAGTCTTGAAAAGTCATTGCCGGAAGAGCTTGTT 	831 AAAGAGATAATTGATAGACGTAAAGACCTTGGTTTGGAGGTACCTAAAGTAAAGAACAT 	891 GTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG 	951 AAAGAGGATCACACCAATCATGATGATGCGTGTGCTCTTCATTTCGCTGTTGCATATTGC	1011 AATGTGAAGACCGCAACAGATCTTTTAAAACTTGATCTTGCCGATGTCAACCATAGGAAT	1071 CCGAGGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCACAATTGATACTA	1131 TCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGAACCGCACTC	1191 ATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTTATATATCCGGGGGGAATGCAAG	1251 CATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGAAGAAGAAGAACGAGAAAAA	1311 ATTCCTAGAGATGTTCCTCCTCTTTGCAGTGGCGCCGATGAATTGAAGATGACGCTG	1371 CTCGATCTTGAAAATAGAGTTGCACTTGCTCAACGTCTTTTTCCAACGGAAGCACAAGCT	1431 GCAATGGAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCT 	1491 GACCGTCTCACTGGTACGAAGACATCACCGGGTGTAAAGATAGCACCTTTCAGAATC	1551 CTAGAAGAGCATCAAAGTAGACTAAAAGGGCTTTCTAAAACCGTGGAACTCGGGAAACGA	1611 TTCTTCCCGCGCTGTTCGGCAGTGCTCGACCAGATTATGAACTGTGAGGACTTGACTCAA
Oy Dp	Qy	Qy Db	Qy Db	QY	Qy Db	Qy Db	oy Op	oy Dp	δ O	oy op	Qy	Qy	Qy Dp	Qy Db	Qy	Qy Db	Qy

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1791 TCCCTGACAGATTCGACTTCTTCCACATCGAAATCAACCGGTGGAAAGAGGGTCTAACCGT 1850
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                                                                                      GAAATACAAGAGACACTAAAGAAGGCCTTTAGTGAGGACAATTTGGAATTAGGAAATTCG 1790
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GENERAL INFORMATION:
APPLICANT: Uknes, Scott
APPLICANT: Hint, Michelle
APPLICANT: Hint, Michelle
APPLICANT: Hint, Michelle
APPLICANT: Ryals, John
TITLE OF INVENTION: ALTERED FORMS OF THE NIMI GENE CONFERRING
TITLE OF INVENTION: ALTERED FORMS OF THE NIMI GENE CONFERENCE
INVENTION: 12 SEASONDENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 5986082artis Corporation
STREET: 3044 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 5986082th Carolina
COUNTRY: USA
ZIP: 27709
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MEDIUM TYPE: Floppy disk
COMPUTER: ELB PC COMPATIBLE
COMPUTER: TEM PC COMPATIBLE
COMPUTER: TEM PC COMPATIBLE
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
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APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08989478 Patent No. 5986082
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                                                                                                                                                                                                                          /product= "1st exon of NIM1"
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                                                                                                                                                                                                                                                                                                                                                      /product= "4th exon of NIM1
                                                      PF/5-21214/P1/CGC1911
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                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                                                                            "3rd
                                                                                                                                                                                                                                                                     "2nd
APPLICATION NUMBER: US 60/035,022 FILING DATE: 10-JAN-1997 ATTORNEY/AGENT INFORMATION:
                             NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REPRENCE/DOCKET NUMBER: PF/5-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5655 base pairs
                                                                                                                                                                                                                                                                                                  LOCATION: 4271..4474
OTHER INFORMATION: /product-
                                                                                                                                                                                                                                                                     /product=
                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                     83.7%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 87.5
Matches 2088; Conservative
                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                 NAME/KEY: exon
LOCATION: 3427..4162
OTHER INFORMATION: /E
                                                                                                                                                                                                       exon 2787..3347
                                                                                                                                                                                                                                                                                                                                NAME/KEY: exon
LOCATION: 4586..486
OTHER INFORMATION:
                                                                                                                                                                                                                            OTHER INFORMATION:
                                                                                                                                                                                                                                                                                         NAME/KEY: exon
                                                                                                                                                                      HYPOTHETICAL: NO ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                      NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                     FEATURE:
NAME/KEY:
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LOCATION:
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3115 TGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTCGGTTGTGA 3174
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                                                   ACCATCTGCATTAAAGCTATGGTTACACATTCATGAATATGTTCTTACTTGAGTACTTGTA
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,685
FILING DATE:
CLASSIFICATION DATA:
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 0-DEC-1996
FILING DATE: 27-DEC-1996
FILING DATE: 37-DEC-1996
FILING DATE: 10-3NA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-3NA 1997
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LOCATION: 4271..4474
OTHER INFORMATION: /product= "3rd exon of NIM1"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 2787..3347
OTHER INFORMATION: /product= "1st exon of NIM1"
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OTHER INFORMATION: /product= "2nd exon of NIM1"
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NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 6031153artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6031153th Carolina
COUNTRY: USA
ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 10-JAN-1997
PRIOR APPLICATION NUMBER: US 08/875,015
APPLICATION NUMBER: US 08/875,015
FILING DATE: 16-JUL-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Meigs, J. Timothy
REGIETRATION UNUBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5
TELECOMMUNICATION INFORMATION:
TELEPAN: (919) 541-8587
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 5655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                  COMPUTER READABLE FORM:
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FEATURE:
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                                      1494 GGTCTCACTGGTACGAAGAAGATCACCGGGTGTAAAGATAGCACCTTTCAGAATCCTA 1553
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TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ryals, John
Friedrich, Leslie
Uknes, Scott
Molina, Antonio
Ruess, Wilhelm
Knauf-Beiter, Gertrude
Kung, Ruth
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Patent No. 6031153
GENERAL INFORMATION:
APPLICANT: Friedrich, Leslie
APPLICANT: Wilnes, Scott
APPLICANT: Molina, Antonio
APPLICANT: Molina, Antonio
APPLICANT: Kness, Wilhelm
APPLICANT: Knauf-Beiter, Gertrude
APPLICANT: Knauf-Beiter, Gertrude
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APPLICANT:
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                                                                                                       TCGATCTTTAACCAAATCCAGTTGATAAGGTCTCTTCGTTGATTAGCAGAGATCTCTTTA
                                                                                                                                                 ATTCTTATGAAATCAGCAGCACTAGTTTCGTCGCTACCGATAACACCGACTCCTATTG
                                                                                                                                                                                  CCAACAGCTTCGAATCCGTCTTTGACTCGCCGGATGATTTCTACAGCGACGCTAAGCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 5655;
                                                                                     Indels
                 of NIM1
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                                                                    DB
                                                                  Score 1760; DE Pred. No. 0; 0; Mismatches
                /product- "4th exon
                                         join(2787..3347,
                                                                    83.7%;
87.5%;
                                                                                     Conservative
          .4866
        LOCATION: 4586..486
OTHER INFORMATION:
FEATURE:
                                                                             Similarity
                                  CDS
                                 NAME/KEY:
LOCATION:
NAME/KEY:
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Matches 2088;
                                                   US-08-996-685-1
                                                                     Query Match
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4614 1361 GAAGACGACACTGCTGAGAAACGACTACAAAAGAAGCAAAGGTACATGGAAATACAAGAG 1742 1181 ATGGAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCTGAC 1493 CAATGCAAGCATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGACAAA 1301 TGTTCGGCAGTGCTCGACCAGATTATGAACTGTGAGGACTTGACTCAACTGGCTTGCGGA TIGCTITIGAAAGAGGAICACACCAAICIAGAIGAIGCGIGIGCCICTICAIITCGCIGII 3715 TIGCTTTTGAAAGAGATCACACCAATCTAGATGCATGCGTGTGCTTTCATTTGCTGTT TTGATACTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGA **ACCGCACTCATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATATCCCGGAG** CGAGAACAAATTCCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAATTGAAG 4195 AATTAAATTTATGTCCTCTCTATTAGGAAACTGAGTGAACTAATGATAACTATTCTTTGT ------AGTTGCACTTGCTCAACGTCTTTTCCAACGGAAGCACAAGCTGCA CGTCTCACTGGTACGAAGAACATCACCGGGTGTAAAGATAGCACCTTTCAGAATCCTA CATCGGACTCCTTATCACAAAAACAAAACTAAATGATCTTTAAACATGGTTTTGTTACT GCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAAACTTGATCTTGCCGATGTCAAC AAGAAACATGTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAG GAAGAGCATCAAAGTAGACTAAAAGCGCTTTCTAAAACC-ATGACGCTGCTCGATCTTGAAAATAG-----4555 3895 4075 1362 4255 4315 4375 1554 4435 1593 4495 1623 4615 1683 942 1062 3835 1122 1182 1242 1302 1388 1388 1434 1494 1593 3655 1002 3955 4135 3595 3775 882 qq g q g 엄 δ g δ qq δy qq οy qq QY g Ω Q Ω Q οy ρp δ Q δý αg οy g ò g δy Ω qq δ ò à ò

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OTHER INFORMATION: /product= "4th exon of NIM1"
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                       DNA (genomic)
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LOCATION: 3427..4162
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NAME/KEY: exon
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APPLICANT: Delaney, Terry
APPLICANT: Delaney, Terry
APPLICANT: Weymann, Kristianna
APPLICANT: Lawton, Kay
APPLICANT: Lawton, Kay
APPLICANT: Ellis, Daniel
APPLICANT: Dinse, Scott
APPLICANT: Jesse, Taco
APPLICANT: Vos, Pieter
TITLE OF INVENTION: GENE ENCODING A PROTEIN INVOLVED IN THE
TITLE OF INVENTION: SIGNAL TRANSDUCTION CASCADE LEADING TO SYSTEMIC ACQUIRED RESIGNABLE OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                  TCGACTTCTTCCACATCGAAATCAACCGGTGGAAAGAGGTCTAACCGTAAACTCTCTCAT 1862
                                                                                                                                                                                     4855 CGTCGTCGGTGAGACTCTTGCCTCTTAGTGTAATTTTGCTGTACCATATAATTCTGTTT 4914
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4675 GAAGACGACACTGCTGAGAAACGACTACAAAAGAAGCAAAGGTACATGGAAATACAAGAG 4734
                             1743 ACACTAAAGAAGGCCTTTAGTGAGGACAATTTGGAATTAGGAAATTCGTCCCTGACAGAT 1802
                                                                                                                    CGTCGTCGGTGAGACTCTTGCCTCTTAGTGTAATTTTTGCTGTACCATATAATTCTGTTT 1922
                                                                                                                                                                                                                                          TCATGATGACTGTAACTGTTTATGTCTATCGTTGGCGTCATATAGTTTCGCTCTTCGTTT 1982
                                                                                                                                                                                                                                                                                                                              1983 IGCAICCIGIGIATTAIIGCIGCAGGIGIGCIICCAAACAAAIGIIGIAACAAITIGAACC
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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ATTORNEY/AGENT INFORMATION:
NAME: Meigs J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: GG 1909
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8687
TELEFAX: (919) 541-8687
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08880179
Patent No. 6091004
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LENGTH: 5655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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STATE: New York
COUNTRY: USA
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Oy 650 bb 3355 ACCATCTGCATTAAGCTATGGTTACACATTCATGAATATCTTCTTACTTGTA 3414 Oy 650 TCAGAGGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGACACATTG 701 Oh 3415 TTTTCTATATTGCACCATTATTGCACACACACACACACAC	702 GTATACTCAAGCTTGCTAATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGATGT 7	762 AAAGAGATTATTGTCAAGTCTAATGTTAGGTTAGGTTAG	822 GAGCTTGTTAAAGAGATAATTGATAGACGTAAAGAGCTTGGTTTGGAGGTACCTAAAGTA 81	882 AAGAAACATGTCTCGAATGTACATAAGGACTTGACTCGGATGATATTGAGTTACTCAG 9	H 6	OY 1002 GCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAAACTTGATCTTGCCGATGTCAAC 1061	Qy 1062 CATAGGAATCCGAGGGGATATACGGTGCTTCATGTTGCTGCGGATGCGGAAGCACCACAA 1121	Qy 1122 TTGATACTATCTCTATTGGAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGA 1181 	Qy 1182 ACCGCACTCATGATGGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATATCCCGGAG 1241	QY 1242 CAATGCAAGCATTCTCTAAAGGCCGACTATGTGTAGAATACTAGAGCAAGAAGACAAA 1301 	OY 1302 CGAGAACAAATTCCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAATTGAAG 1361	OY 1362 ATGACGCTCCATCTTGAAATAG	Оу 1388 1387	4	Oy 1388AGTTGCACTTGCTCAACGTCTTTTCCAACGAAGCACGCAAGGTGCA 1433 Db 4255 GTCGTCCACTGTTTAGTTGCACTTGCTCAACGTCTTTTCCAACGGAAGCAAGC	OY 1434 ATGCAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTGACTGGCTTGAGCTCGACCTGAC 1493	Qy 1494 CGTCTCACTGGTACGAAGAACATCACCGGGTGTAAAGATAGCACCTTTCAGAATCCTA 1553	Qy 1554 GAAGAGCATCAAAGTAGACTAAAAGCGCTTTCTAAAACC

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ACCATCTGCATTAAGCTATGGTTACACATTCATGAATATGTTCTTACTTGAGTACTTGTA 3148
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                                                                                                                                                                                                                                                        Length 9919;
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                                                                                                                                                                                                                                                     Score 1760; DF
Pred. No. 0;
0; Mismatches
SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,179
                              FILING DATE:
CLASSTRICATION: 800
ATORNEY/AGENT INFORMATION:
NAME: Me19s, J. Timochy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: GG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEPHONE: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9919 base pairs
TYPE: nucleic acid
STRANDENESS: Single
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Timothy
Ten: 38,241
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                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                       Query Match 83.7%;
Best Local Similarity 87.5%;
Matches 2088; Conservative
                                                                                                                                                                                        linear
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US-08-880-179-1
                                                                                                                                                                                       TOPOLOGY:
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Query Match 76.3
Best Local Similarity 100.
Matches 1605; Conservative
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                                                                     TGTTCGGCAGTGCTCGACCAGATTATGAACTGTGAGGACTTGACTCAACTGGCTTGCGGA
                                                                                                                                                                 ACACTAAAGAAGGCCTTTAGTGAGGACAATTTGGAATTAGGAAATTCGTCCCTGACAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Uknes, Scott
APPLICANT: Uknes, Michelle
APPLICANT: Hunt, Michelle
APPLICANT: Steiner, Henry-York
APPLICANT: Steiner, Henry-York
APPLICANT: Ryals, John
TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                      AATGGTATACAGATTTGTAATATATTTTATGTACATCAACAATAA 2088
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: No. 5986082artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 5986082th Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRION APPLICATION DATA:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/08989478 Patent No. 5986082 GENERAL INFORMATION:
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241 GCTAAGCTTGTTCTCTCCCGACGCCGGGAAGTTTCTTTCCACCGGTGCGTTTGTCAGCC

411 ACCGCCGCCGTGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCCAT

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111 GGATTCGCCGATTCTTATGAAATCAGCAGCACTAGTTTCGTCGCTACCGATAACACCGAC 170

GATCTCTTTAATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACCACCATTGAT 110

300 410 480

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/product= "Altered form of NIM1" /note= "C-terminal deletion compared to wild-type NIM1."
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100.0%; Pred. No. 0;
iive 0; Mismatches
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5
TELECOMUNICATION INFORMATION:
TELEPHONE: (919) 541-8687
TELERAX: (919) 541-8687
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1608 base pairs
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STRANDEDNESS: single
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COTHER INFORMATION:

COTHER INFORMATION:

CS-08-989-478-11
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1561 TTCTTCCCGCGCTGTTCGGCAGTGCTCGACCAGATTATGAACTGT 1605
                                                                                                                                                                                                                                                                                     APPLICANT: Kessmann, Helmut
APPLICANT: Oostendorp, Michael
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF/5-21215/P1/CGC1912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,378
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
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FILING DATE: 27-DEC-196
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
PRIOR APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
PRIOR APPLICATION NUMBER: US 60/035,022
APPLICATION NUMBER: US 60/035,022
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                                                                                                                                                                                                                              Ruess, Wilhelm
Knauf-Beiter, Gertrude
Kung, Ruth
Kessmann, Helmut
                                                                                             Sequence 11, Application US/08996685
Patent No. 6031153
                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
21P: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MC
SOFTWARE: Patent
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                                                                                                                                                                       Friedrich, Leslie
Uknes, Scott
Molina, Antonio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (919) 541-8587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 16-JUL-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1608 base pairs TYPE: nucleic acid
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                                                                                                                                                      Ryals, John
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                                                                                                                              GENERAL INFORMATION:
APPLICANT: Ryals,
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APPLICANT:
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APPLICANT:
                                                           RESULT 10
US-08-996-685-11
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                                                                                                                                    CAGAGGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTATACTC
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CATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGACAAACGAGAACAA
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                                                1071 CCGAGGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAATTGATACTA
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APPLICANT: Hunt, Michelle
APPLICANT: Hunt, Michelle
APPLICANT: Steiner, Henry-York
APPLICANT: Ryals, John
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
MUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5986082artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                          1611 TTCTTCCCGCGCTGTTCGGCAGTGCTCGACCAGATTATGAACTGT 1655
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No. 5986082th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-989-478-9; Sequence 9, Application US/08989478; Patent No. 5986082
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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                                                    /product= "Altered form of NIM1" /note= "C-terminal deletion compared
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Pred. No. 0
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Best Local Similarity 100.0%;
Matches 1605; Conservative 0
 single
                                   NAME/KEY: CDS
LOCATION: 43..1608
OTHER INFORMATION: /
STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                          US-08-996-685-11
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PatentIn Release #1.0, Version #1.30
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99.9%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                   APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                 APPLICATION NUMBER: US 60/034,379 FILING DATE: 27-DEC-1996
                     US/08/989,478
                                                                                                                                    US 60/034,382
                                                                   60/033,177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sednence.
                                                                                                                                                                                                                                                                         NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKTY NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                     TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 1597 base pairs
                                                               APPLICATION NUMBER: US 6C FILING DATE: 13-DEC-1996 PRIOR APPLICATION DATA:
                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 66
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 99.3
Matches 1594; Conservative
          DATA
                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                          PRIOR APPLICATION DATA:
                                                     PRIOR APPLICATION DATA:
        CURRENT APPLICATION DA APPLICATION NUMBER: FILING DATE:
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                     TTTTGAAAGAGGATCACCAATCTAGATGATGCGTGTGCTCTTCATTTCGCTGTTGCAT
                                                                                                                                                                                 ATTGCAATGTGAAGACCGCAACAGATCTTTTAAAACTTGATCTTGCCGATGTCAACCATA
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TTGTTAAAGAGATAATTGATAGACGTAAAGAGCTTGGTTTGGAGGTACCTAAAGAAGA
                                                                            AACATGTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAGTTGC
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Query Match
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MN-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,685
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: OSSTENDORP, MICHAEL TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS NUMBER OF SEQUENCES: 32
                                                                                                                        2026 TIGIAACAATITGAACCAATGGIATACAGAITIGIA 2061
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: No. 6031153artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6031153th Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
PRIOR APPLICATION NUMBER: US 60/034,378
FILING DATE: 27-DEC-1996
FILING DATE: 10-0AN-1997
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APPLICATION NUMBER: US 08/875,015
FILING DATE: 16-JUL-1997
ATTORNEY/AGENT INFORMATION:
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10-JAN-1997
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FILING DATE: 10-JAN-1997
                                                                                                                                                                                                                                                                          Friedrich, Leslie
Uknes, Scott
Molina, Antonio
Ruess, Wilhelm
Knauf-Beiter, Gertrude
                                                                                                                                                                                                               Sequence 9, Application US/08996685 Patent No. 6031153
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APPLICANT: Kessmann, Helmut
APPLICANT: Oostendorp, Micha
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APPLICANT: Ryals,
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APPLICANT:
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/product= "Altered form of NIM1" /note= "N-terminal deletion compared to wild-type NIM1 sequence."
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                                                                                                                                                                                                                                                                                                                                                                                                                                            466 TCGATTCGGTTGTGTGTTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCCGCCTA 525
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               PF/5-21215/P1/CGC1912
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                                                                                                                                                                                                                                                                                                                                                                   Score 1592.8;
                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0;
           REFERENCE/DOCKET NUMBER: PF/5
TELECOMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1597 base pairs
38,241
                                                                                                                                                                                                                                                                                                                                                                   75.78;
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Matches 1594; Conservative
REGISTRATION NUMBER:
                                                                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                         CTHER INFORMATION:
US-08-996-685-9
                                                                                                                                                                                                                                                       LOCATION: 1..1410
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                MOLECULE TYPE: CDNA
                                                                                                                                                                                  linear
                                                                                                                                                                                                                     FEATURE:
NAME/KEY: CDS
                                                                                                                                            TYPE: nucleic STRANDEDNESS:
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466 TCGATTCGGTTGTGACTGTTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCCGCA 525
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/note= "N-terminal/C-terminal chimera.
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                                                                                                                                                                                             Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFEX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.5%; Score 1188.4; 99.9%; Pred. No. 0; iive 0; Mismatches
                     Corporation
                                                                                                                                                                                                                                                                       PRICRATION DATA:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRICRATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRICRA PAPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRICRA PAPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRICRA APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
APPLICATION NUMBER: US 60/034,730
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 10-JAN-1997

FRICK APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997

FRICK APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022

FILING DATE: 10-JAN-1997

APPLICATION NUMBER: US 60/035,022

ATTORNEY/AGENT INFORMATION:
                                                                                                                                     MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIDLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PALENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                            US/08/989,478
STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 5986082th Carolina ZIP: 777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
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TYPE: nucleic acid
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Matches 1189; Conservative
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FILING DATE:
CLASSIFICATION:
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OTHER INFORMATION:
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LOCATION: 1..1
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                                                                                                   27709
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                                    781
              1246 GCAAGCATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGACAAAGGAG
                                                                                   1366 CGCTGCTCGATCTTGAAATAGAGTTGCACTTGCTCAACGTCTTTTTCCAACGGAAGCAC
                                                                                                                                                                                                                                                                         1426 AAGCTGCAATGGAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTGACTAGCCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1666 CTCAACTGGGTTGCGGAGAAGACGACACTGCTGAGAAACGACTACAAAAGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Uknes, Scott
APPLICANT: Uknes, Scott
APPLICANT: Steiner, Michelle
APPLICANT: Steiner, Henry-York
APPLICANT: Ryals, John
TITLE OF INVENTION: ALTERED FORMS OF THE NIMI GENE CONFERRING
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2026 TIGIAACAATITGAACCAATGGIATACAGATITGIA 2061
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Uknes, Scott

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APPLICANT
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706 TACTCAAGCTTGCTAATATATGTGTAAAGCTTGTATGAAGCTATTGGATAGATGTAAAG
                   242 TACTCAAGCTTGCTAATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGATGTAAAG
                                                                                                                                   826 TTGTTAAAGAGATAATTGATAGACGTAAAGAGCTTGGTTTGGAGGTACCTAAAGTAAAGA
                                                                                                                                                                                                                                                                                                       482 TTTTGAAAGAGGATCACAACCTAGATGATGCGTGTGCTCTTCATTTCGCTGTTGCAT
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                                                                  AGATTATTGTCAAGTCTAATGTAGATATGGTTAGTCTTGAAAAGTCATTGCCGGAAGAGC
                                                                                                                                                                                                    AACATGTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAGTTGC
                                                                                    1606 AACGATTCTTCCCGCGCTGTTCGGCAGTCCTCGACCAGATTATGAACTGT 1655
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US-08-996-685-13
Sequence 13, Application US/08996685;
Patent No. 6031153
GENERAL INFORMATION:
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APPLICANT: Ryals, John APPLICANT: Friedrich, Leslie

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/product= "Altered form of NIM1"
/note= "N-terminal/C-terminal chimera."
                                                                                                     APPLICANT: Oostendorp, Michael TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 060/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 050/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATE: 050/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATE: 150-JAN-1997
FILING DATE: 10-JAN-1997
FILING DATE: 10-JAN-1997
FILING DATE: 10-JAN-1997
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/875,015
FILING DATE: 16-JUL-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/034,378
FILING DATE: 27-DEC-1996
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,024
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/996,685
Molina, Antonio
Ruess, Wilhelm
Knauf-Beiter, Gertrude
                                                                                                                                                                                                                    STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6031153th Carolina
COUNTRY: USA
                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6031153artis
                                                                                                                                                                                                                                                                                                                                                          : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (919) 541-8587
TELEPAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
                                                                                       Kessmann, Helmut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1194 base pairs
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CTHER INFORMATION: /
CTHER INFORMATION: /
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                                                                Kung, Ruth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                              27709
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                                                              APPLICANT:
APPLICANT:
APPLICANT:
                    APPLICANT:
APPLICANT:
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1022 AGCCTGACCGTCTCACTGGTACGAAGAACATCACCGGGTGTAAAGATAGCACCTTTCA 1081
                                                                            1082 GAATCCTAGAAGAGCATCAAAGTAGACTAAAAGCGCTTTCTAAAACCGTGGAACTCGGGA
                                              1546 GAATCCTAGAAGAGCATCAAAGTAGACTAAAAGCGCTTTCTAAAACCGTGGAACTCGGGA
                                                                                                                                                                                                                                                ENERAL INFORMALLON.
APPLICANT: Uknes, Scott
APPLICANT: Unternational Michelle
APPLICANT: Steiner, Henry-York
APPLICANT: Steiner, Henry-York
APPLICANT: Ryals, John
TITLE OF INVENTION: ALTERED FORMS OF THE NIMI GENE CONFERRING
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
                                                                                                                           1142 AACGATTCTTCCCGCGCTGTTCGGCAGTGCTCGACAGATTATGAACTGT 1191
                                                                                                           1606 AACGATTCTTCCCGCGCTGTTCGGCAGTGCTCGACCAGATTATGAACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF/5-21214/P1/CGC1911
                                                                                                                                                                                                                                                                                                                                                                                        SSEE: No. 5986082artis Corporation
F: 3054 Cornwalls Road
Fesearch Triangle Park
No. 5986082th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/034,730 FILING DATE: 10-JAN-1997 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021 FILING DATE: 10-JAN-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/989,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                   Sequence 15, Application US/08989478 Patent No. 5986082 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : LULEHONE: (919) 541-8587

TELEFAX: (919) 541-8689

INFORMATION FOR SEG ID NO: 15: SEGUENCE CHARACTERISTICS: LENGTH: 786 base pairs TYPE: nucleic acid TYPE: nucleic acid TYPE: nucleic acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PF
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 27709
COMPUTER READABLE FORM:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
STREET: 30!
CITY: Resec
                                                                                                                                                                                                    US-08-989-478-15
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                                 Gaps
                                                                                           61
                                                                                                                                                                                                                                                                                                        302 AGATTATTGTCAAGTCTAATGTAGATATGGTTAGTCTTGAAAAGTCATTGCCGGAAGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         946 TTTTGAAAGAGGATCACACCAATCTAGATGATGCGTGTGCTCTTCATTTCGCTGTTGCAT
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 Length 1194;
                                ;
0
                                Indels
                                1;
 DB 3;
56.5%; Score 1188.4; 99.9%; Pred. No. 0;
                              0; Mismatches
                              Matches 1189; Conservative
                Similarity
 Query Match
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                                                    Length 786;
                                                                      Indels
                  /product= "Altered form of NIM1"
/note= "Ankyrin domains of NIM1."
                                                    Ouery Match
37.1%; Score 781.4; DB 2;
Best Local Similarity 99.9%; Pred. No. 3.3e-213;
Matches 782; Conservative 0; Mismatches 1;
HAME/KEY: CDS
CCATION: 1..786
COTHER INFORMATION:
CTHER INFORMATION:
US-08-989-478-15
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Search completed: October 8, 2002, 01:23:14 Job time : 117.761 secs BE6306 F18D8TF IGF BW0745943 WSL_38_H0 BE435499 EST406577 BE918569 OVL_8_E08 BC521476 10-59 Ste BF657743 OV2_17_E0 AW22846 EST306916 AL372473 MTBA31C01 BH594302 BOHOK24TR BW307942 EST306916 BM307942 EST306916 BM324012 PR013BDSR BW324012 PR013BDSR BW324012 PR013BDSR BW324012 PR013BDSR BW324012 PR013BDSR BW36196 PR1_31_F0 BE8101977 ST23408.9 BE8101977 ST23408.9 BC526883 40-96 Ste BC526883 40-96 Ste BM310424 EST528464 AW310962 SG31BD2.x AN310962 SG31BD2.x AN310983 CG55R300

AW745943 BE023215 BE023215 BE03221676 BE51476 BE521476 BE521473 AM622846 AL42277 AM622846 AL42277 AM687759 BE3324012 BE36196 BE36197 BE36197

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RESULT
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                                     7, 2002, 21:32:09; Search time 1642.95 Seconds (without alignments) 17284.510 Million cell updates/sec
                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                             GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                        13736207 seqs, 6748477542 residues
                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                           - nucleic search, using sw model
                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                   gb_est2:*
gb_htc:*
gb_gss:*
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em_gss_inv:*
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Maximum DB seq length: 2000000000
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                          OM nucleic
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ALIGNMENTS

	Description	AV551266 AV551266	AT997958 701671677	AA395706 28108 Lam	AV557971 AV557971	BH525927 BOGTOOATE	BH602085 BOHKB84TF	T22612 4620 Lambda	BH211724 SALK 0065	AW160235 EST290093	BG464249 EM1 71 D1	BM111027 EST558563	BG124935 EST470581	ВН602094 ВОНКВАТВ	BG59808 EST503708		AW399343 EST309843	BG526766 63-52 Ste
SUMMARIES	ID	AV551266	A1997958	AA395706	AV557971	BH525927	BH602085	T22612	BH211724	AW160235	BG464249	BM111027	BG124935	BH602094	BG598808	BE493178	AW399343	BG526766
	DB	6	σ	6	6	12	12	10	12	6	10	10	10	12	10	10	σ	10
	Query Match Length DB	573	495	470	338	772	799	258	463	613	614	700	654	785	667	455	450	744
æ	Query	27.2	23.4	18.0	14.6	14.5	11.2	11.0	10.9	10.1	10.0	8.9	8.9	8.2	7.8	7.6	7.3	7.3
	Score	573	493	378.6	307.8	305.2	236	231.2	228.8	212.8	211.4	187.8	186.8	172.2	163.2	160.6	154.2	152.8
	Result No.	1	c 5	æ	C 4	c 2	9 0	7	8 0	6 U	10	11	12	13	14	15	16	17

	RESULT I	
_	AV551266	
_	LOCUS	AV551266 573 bp mRNA linear EST 06-SEP-2000
_	DEFINITION	thaliana roots Columbia Arabido
_		cDNA clone RZ123e05R 5', mRNA sequence.
	ACCESSION	
	VERSION	AV551266.1 GI:8722679
	KEYWORDS	EST.
	SOURCE	thale cress.
	ORGANISM	Arabidopsis thaliana
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
		Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
	REFERENCE	1 (bases 1 to 573)
	AUTHORS	Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
	TITLE	A large scale analysis of cDNA in Arabidopsis thaliana: Generation
_		of 12,028 non-redundant expressed sequence tags from normalized and
_		size-selected cDNA libraries
	JOURNAL	DNA Res. 7, 175-180 (2000)
	MEDLINE	20363093
	COMMENT	Contact: Erika Asamizu
		The First Laboratory for Plant Gene Research
		Kazusa DNA Research Institute
		Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
-		Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
	FEATURES	Location/Qualifiers
_	source	1573
		/organism="Arabidopsis thaliana"
_		/strain="Columbia"
_		/db_xref="taxon:3702"
_		/clone="RZ123e05R"
		/clone_lib="Arabidopsis thaliana roots Columbia"
		/tissue_type="roots"
		/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
_		Xhoi"
	BASE COUNT ORIGIN	181 a 104 c 137 g 151 t
	Query Match	27.28; s
		TOO.O.S. FIEU. NO.

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/issue_type="rosette"
//issue_type="rosette"
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99.6%; Pred. No. 1.4e-83;
tive 0; Mismatches 2;

    .495
    /organism="Arabidopsis tha
/cultivar="Columbia Col-0"
/db_xref="taxon:3702"

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Contact: David Smoller, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                           AGGATCACACCAATCTAGATGATGCGTGTGTGCTTTACATTTCGCTGTTGCATATTGCAATG 1014
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                                                                                                                                                                                                                                                                                              121 CGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTGAAAG 180
                                                                                                                                                                                                                                                                     CGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTGAAAG 954
Gaps
                                                                                                      1 TCAAGTCTAATGTAGATATGGTTAGTCTTGAAAAGTCATTGCCGGAAGAGCTTGTTAAAG 60
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Location/Qualifiers
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Tel: 877-577-2733
Fax: 314-427-3324
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us-08-908-884-2.rst

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1 (bases 1 to 338)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
Alarge scale analysis of cDNA in Arabidopsis thaliana: Generation of 12.028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
                                                                                               AV557971 Arabidopsis thaliana green siliques Columbia Arabidopsis thaliana green siliques Columbia Arabidopsis thaliana cDNA clone SQ085f0lF 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS 13-DEC-2001
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="Columbia"
/db_xref="taxon:3702"
/clone="$Q085f01F"
/clone_lib="Arabidopsis thaliana green siliques Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="green'siliques"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
xhoI"
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Kazusa DNA Research Institute
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    .338
    /organism="Arabidopsis thaliana"

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Matches 309; Conserv
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AV557971/c
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 470)
Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anote—"Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings: 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA linears were directionally cloned with Sal-Not arms using
                                                                                                                                       clones
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                                                                                                             Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA (Plant Physiol. 106, 1241-1255 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 GAAAGAGGTCTAAACGTAAACTCTCTCATCGTCGGTGAGACTCTTGCCTCTTAGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                /organism="Arabidopsis thaliana"
/strain="var columbia"
/db_xref="taxon:3702"
/clone="9905XP"
/clone_lib="Lambda-PRL2"
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                                                                                                                                                                                                           MSU-DOE Plant Research Laboratory Michigan State University
                                                                                                                                                                                                                                                                                Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@thm.cl.msu.edu
Seq primer: M13-21 dye primer.
                                                                                                                                                                                                                                                                                                                                            r: M13 -21 dye primer.
Location/Qualifiers
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                                                                                                                                                                                         Contact: Thomas Newman
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93.3%;
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101 c
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BH602085 799 bp DNA linear GSS 15-DEC-2001
BOHKB84TF BOHK Brassica oleracea genomic clone BOHKB84, DNA
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Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1591 CCGTGGAACTCGGGAAACGATTCTT-CCCGCGCTGTTCGGCAGTGCTCGACCAGATTATG 1649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1650 AACTGTGAGGACTTGACTCAACTGGCTTGCGGAGAAGACGACACTGCTGAGAACGACTA 1709
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/note="Vector: pHOSI; Site_l: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOSI using BstXI linkers"
164 c 165 g 219 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        haploid provided by Tom Osborn
                                                                        232 CTACTCCTGATGAATTGAGGATGAGGCTGCTCTATCTTGAAAACAGAGGT 183
                                                                                                                                                                                                                                                                                                                                                                                        Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other_GSSS: BOHKB84TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Drive, Rockville, MD 20850, USA
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/organism="Brassica oleracea"
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/clone="BOHKB84"
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                                                                                                                                                                                                                                                  BH602085.1 GI:17854531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cdtown@tigr.org
DNA is from a doubled |
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Class: sheared ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 301-838-3523
Fax: 301-838-0208
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                                                                                 Brassica oleracea.
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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/strain="T01000DH3"
/db_xref="taxon:3712"
/clone_lib="BoGT004"
/clone_lib="BoGT"
/note="Vector: pH0S1; Site_l: BstXI; 2-3 kb sheared
genomic DNA inserted into pH0S1 using BstXI linkers"
187 c 176 g 210 t
BOGTO04TF BOGT Brassica oleracea genomic clone BOGTO04, DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 772;
                                                                                                                                                                                                                                                                                                712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-88-3523
Fax: 301-838-0268
Email: coltown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn. Seq primer: TF
Class: Basred ends.
Location/Qualifiers
                                                                                                                                                                         1 (bases 1 to 772)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 305.2; DB 12;
Pred. No. 5e-48;
0; Mismatches 178;
                                                   BH525927.1 GI:17734012
                                                                                                                                                                                                                                                  Other GSSs: BOGTO04TR
Contact: Chris Town
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SALK_006564 Arabidopsis thallana TDNA insertion lines Arabidopsis thallana genomic clone SALK_006564, DNA sequence.
BH211724
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Alonso,J.W., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Heller,C., Kim,C.J., Joske,A., Koesema,E., Meyers,M.C., Parker,H., Prednis,L., Shinn,P., Stevenson,D.K., Zimmerman,J. and Ecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="SALK_00564"
/clone="SALK_00564"
/clone=lib="Arabidopsis thaliana TDNA insertion lines"
/clone=lib="Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

116 c 88 g 127 t
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                                                                                                                TGATACTATCTCTATTGGAAAAGGTGCAAG-TGCATCAGAACCAACTTTGGAAGGTAGA 1181
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                         ATAGGAATCCGAGGGGATATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAAT 1122
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                                              181 TTATACTATCTCTATTGGAAAAAGGTGCAAGTTGCATCAGAAGCAACTTTGGAAGGTAGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is single pass sequence recovered from the left border of TDNA. This sequence lies within an intron of At4926120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
/strain="Columbia 0"
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Pred. No. 1.6e-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.9%;
72.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_1995377.
/clone_lib="Lambda-PRL2"
/clone_lib="Lambda-PRL2"
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems; 2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 258)
Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel,E. and Somerville,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
                                                                                                                                                                                                                                                                                             T22612
4620 Lambda-PRL2 Arabidopsis thaliana cDNA clone 9905T7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                       1947 TCTATCGTTGGC---GTCATATAGTTTCGCTCTTCGTTTTGCATCCTGTGTATT--ATTG 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               943 IGCTTTTGAAAGAGGATCACAACCAATCTAGATGATGCGTGTGCTCTTTCATTTCGCTGTTG 1002
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463 GGGTAATATTTGATGTACCATATATATATTTTGAGTTATCATGTGTCTTAGTGTCTCTG 404
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MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
                                                                                                                                2002 CIGCAGGIGIGCTICAAACAAAIGTIGIAACAAITIGAACCAAIGGIAIACAGAIT 2057
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On Nov 6, 1997 this sequence version replaced gi:932513
                                                                                                                                                        DB 10; Length 258;
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/organism="Arabidopsis thaliana"
/strain="var columbia"
/db_xref="taxon:3702"
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94.6%; Pred. No. 6.2e-34;
ive 0; Mismatches 13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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High quality sequence stop: 610
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   Conservative
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Fax: 706 542 1805
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BG464249.1
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XhoI; Leaves of various stages were shaken in liquid
nitrogen, shearing off trichomes. This procedure yielded a
mixture of cells highly enriched for trichomes, with minor
contamination by other types of leaf cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 18-MAY-2001
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lycopersicon.

1 (bases 1 to 613)

1 (bases 1 to 613)

Lidang, J., Vrebalov, J., White, R., Matern, A.L., Lakey, J., Holt, I.E. Liang, F., Hansen, T.S., Upton, J., Ronning, C.M., Craven, M.B., Fujii (C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and Glovannoni, J.
Generation of ESTs from wild tomato (Lycopersicon pennellii)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST290093 L. pennellii trichome, Cornell University Lycopersicon pennellii cDNA clone cLPTII9 similar to A. thaliana transcription factor inhibitor I kappa B homolog, mRNA sequence.
                                                                                                                                                                                                        TGTGTAGAAATACTAGAGCAAGAAGACAAACGAGAACAAAT---TCCTAGAGATGTTCCT 1328
                                                                                                                                                                                                                                                                          CCCTCTTTTGCAGTGGCGGCCGATGAATTGAAGATGACGCTGCTCGATCTTGAAAATAGA 1388
                                                                                                                                    ATGCCGGTTGAATGTAATATATCCCGGAGCAATGCAAGCATTCTCTCAAAGGCCGACTA 1271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="L. pennellii trichome, Cornell University"
//tissue_type="trichome"
/dev_stage="mixed stages"
/lab_host="SOLR"
                                                                                                                                                           223 AAAGCGGATGACTACAAAACTAGTACGAGGACGGTACGCCTTCTCTGAAAGGCGGATTA 164
                   44
                                                                                    CATGTTGCTGCGATGCGGAAGGAGCCACAATTGATACTATCTCTATTGGAAAAAGGTGCA
                                                                  1152 AGTGCATCAGAAGCAACTTTGGAAGGTAGAACCGCACTCATGATCGCAAAACAAGCCACT
                                                                                                                                                                                                                                                                                            103 CTTTCTCTTCCAGTAACTCCAGAGGAGTTGAGGATGAGGTTGCTCTATTATGAAAACCCGA
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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/db_xref="taxon:28526"
/clone="cLPT119"
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Pred. No. 1.7e-30;
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Lycopersicon pennellii
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                                                                                                                                                                                                                                                                                                                                            GTTGCACTTGCT 1400
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AUTHORS
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BG464249 614 bp mRNA linear EST 20-MAR-2001 EM1_71_D12.b1_A002 Embryo 1 (EM1) Sorghum bicolor cDNA, mRNA sequence.
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1 (bases 1 to 614)

1 (bases 1 to 614)

1 Refd.S.P., Cordonnier-Pratt,M.-M., Gingle,A. and Pratt,L.H.

An EST database from Sorghum: developing embryos

Unpublished (2000)
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1707 CTACAAAAGAAGCAAAGGTACATGGAAATACAAGAGACACTAAAGAAGGCCTTTAGTGAG 1766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1587 AAAACCGTGGAACTCGGGAAACGATTCTTCCGGGGCTGTTCGGCAGTGCTCGACCAGATT 1646
                                                                                                                               1347 GCCGATGAATTGAAGATGACGCTGCTCGATCTTGAAAATAGAGTTGCACTTGCTCAACGT 1406
                                                                                                                                                                                                                                                                                                                                                                                                    1467 ITCATAGTGACTAGCCTCGAGCCTGACCGTCTCACTGGTACGAAGAGAACATCACCGGGT 1526
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                                                                                                                                                                                                                                                                                                                                 492 CTTTTTCCCATGGAAGCAAAGTTGCAATGGACATTGCTCAAGTTGATGGCACGTCTGAA 433
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                                                                                                                                                                      195 CAACTGAAGAAGCAAAGGTACATGGAACTTCCAAGAAATTTTGTCTAAAGCATTCACGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1527 GTAAAGATAGCACCTTTCAGAATCCTAGAAGAGCATCAAAGTAGACTAAAAGCGCTTTCT
                                                                                                                                                                                                                                                                     1407 CTTTTTCCAACGGAAGCACAAGCTGCAATGGAGATCGCCGAAATGAAGGGAACATGTGAG
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Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Sorghum bicolor"
/db_xref="taxon:4558"
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/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: Mobils supplier: Cornell University, Tanksley lab; sequencing: The Institute for Genomic Research. Roots were isolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATACGGTGCTTCATGTTGCTGCGATGCGGAAGGAGCCACAATTGATACTATTGG 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1021 CCGCAACAGATCTTTTAAAACTTGATCTTGCCGATGTCAACCATAGGAATCCGAGGGGAT 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1141 AAAAAGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGAACCGCACTCATGATCGCAA 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1201 AACAAGCCACTATGGCGGTTGAATGTAATATATCCGGGAGCAATGCAAGCATTCTCTCA 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGTTACTGAGGTTCTTGGACTGGGTGTTGCTAATGTCAACCTTCGGAATACAGGTGGTT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Utterback, T., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., TankRaley, S. and Baker, B.
Generation of ESTs from potato roots
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 TATACAAGGCATTGGATTCAGATGATGTTGAACTTGTCAAGCTTCTACTTAATGAGTCTG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  901 TACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTGAAAGAGGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAATTGAAGATGACGCTGCTCGATCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 700;
                                                                                                                                                                                                                               1. 700
/organism="Solanum tuberosum"
/oultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cpRollOG3"
/clone=lib="potato roots"
/tissue_type="roots"
/dev_stage="in vitro grown stem cuttings"
/lab_host="SOLR"
                                                                               Contact: Research Genetics, Libraries Division Tel: 1-800-711-6195 Email: cdnadersgen.com For clone info: please contact Research Genetics, I Division tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 187.8; DB 10;
Pred. No. 8.9e-26;
0; Mismatches 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA
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Best Local Simil
Matches 306; C
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                                                                                                                                                                                                                                  source
                                        TITLE
JOURNAL
COMMENT
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LOCUS
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                 /note="Organ: Embryos germinated for 24 hr; Vector: Baltescript II from Lambda Zap II; Site_1: XhoI; Site_2: ECORI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were
                                                                                                                                                                                                                             ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 700)
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van der Hoeven,R., Sun,H., Karamycheva,S.A., Tsai,J., Van Aken,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTGTAGAAATACTAGAGCAAGAAGACGAGAACAACAAGAATTCCTAGAGATGTTCCTCCC 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1152 AGTGCATCAGAAGCAACTTTGGAAGGTAGAACCGCACTCATGATCGCAAAACAAGCCACT 1211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         428 AATCATGGGGATTACTTTGGGCCTACTGAGGATGGAAAGCCTTCTCCTAAAGATAAGATAA 487
                                                                                                                                                                                                                                                                  804 GAAAAGTCATTGCCGGAAGAGCTTGTTAAAGAGATAATTGATAGACGTAAAAGAGCTTGGT 863
                                                                                                                                                                                                                                                                                                                                                      ----AAACATGTCTCGAATGTACATAAGGCA 911
                                                                                                                                                                                                                                                                                                                                                                                           68 TTAGTITTACCAGAGGACAAGGGCTTCCCTAACATACATGTAAGAAGAGTACACAGGGCG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                 912 CTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTTGAAAGAGGATCACCAATCTA 971
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                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                       8 GAGAAGGCATTGCCTCCAGATGTTGTCAAAGCAATTGTTGATGCAAGGCTAAGTCTTGGA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             488 TGTATTGAGATACTAGAGCAAGCTGAAAGAAGGACCCACCATCTTGGAGAAGCATCAGTT
                                                                                                                                                                                                                             12;
                                                                                                                                                                                       DB 10; Length 614;
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                  10.0%; Score 211.4; DB 10;
llarity 60.8%; Pred. No. 3.1e-30;
Conservative 0; Mismatches 226;
/clone_lib="Embryo 1 (EM1)"
                                                                                                     prepared by mass excision."
                                                                                                                      146 g
                                                                                                                                                                                                                                                                                                                                                    TTGGAGGTACCTAAAGTAAAG-----
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Solanum tuberosum
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Gaps

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EST 31-JAN-2001

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/strain="TO1000DH3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                    Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled ha
Seq primer: TR
Class: sheared ends.
                                                                                                                             BH602094.1 GI:17854540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.2%;
74.7%;
                                                                                                                                                                                                                                                                                                                         Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 74.73
Matches 216; Conservative
                                                                                                                                                               Brassica oleracea
                                                                                                                                                                               Brassica oleracea
                                                                                 BOHKB84TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217
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ORIGIN
                                                                               DEFINITION
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COMMENT
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EST470581 tomato shoot/meristem Lycopersicon esculentum cDNA clone cTOF7K1 5' sequence, mRNA sequence.
BG124935
                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /hote-weetor: pBluescript SK(-); Site_1: EcoR1; Site_2: Xhol: Small expanding leaves from the growing tip were taken from greenhouse plants (4-6wks old TA496). Tissue was immediately frozen in liquid nitrogen."
                                                                                                                                                                            1 (bases 1 to 654)

van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Utterback, T.,
Hansen, C., Ronning, C. and Tanksley, S.
Generation of ESTs from tomato shoot/meristem tissue
Unpublished (2001)
Contact: CUGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1353 GAATTGAAGATGACGCTGCTCGATCTTGAAAATAGAGTTGCACTTGCTCAACGTCTTTTT 1412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGAGGACTTGACTCAACTGGCTTGCGGAGAAGACGACACTGCTGAGAACGACTACAA 1712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGAAGCAAAGGTACATGGAAATACAAGAGACACTAAAAGAAGGCCTTTAGTGAGGACAAT 1772
                                                                                                                                                                                                                                                                                                                                                                                                                /clone="crOF7K1"
/clone_lib="tomato shoot/meristem"
/tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 CTGCCTAGCAT---GAGGAAGAAGAAGATAGCTGATGCACAGAGGACAACAGGGGATTTGAAC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 GCTGATGACTTGTCTGAGATAGCTTACATGGGGAACGATACAGTAGAAGAGGGTCAACTG 358
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                                                                                                                                                                                                                                                                                      Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
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0; Mismatches 167; Indels
                                                                                                                                                                                                                                                                                                                                                                    /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
                                                                                                                                                                                                                                                                          Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 186.8;
                                                                                                Lycopersicon esculentum
                                                BG124935.1 GI:12625123
EST.
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63.8%;
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                                                                                                                                                             Lycopersicon
                                                                                 tomato
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   DEFINITION
                                                                               SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                            REFERENCE
AUTHORS
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JOURNAL
COMMENT
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                                                VERSION
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EST503708 cSTS Solanum tuberosum cDNA clone cSTS22E2 5' sequence, mRNA sequence.
BG598808.1 GI:13618649
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GSS 15-DEC-2001
                                                                                                                                                                                   Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots; Sosidae; eurosida II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 785)

Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other_GSSS; BOHKB84TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   621 TTCAAGATCCCTGAATTAATTACTCTCTATCAGAGGCACTTATTGGACGTTGTAGACAAA 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      681 GTTGTTATAGAGGACACATTGGTTATACTCAAGCTTGCTAATATATGTGGTAAAGCTTGT 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  741 ATGAAGCTATTGGATAGATGTAAAGAGATTATTGTCAAGTCTAATGTAGATATGGTTAGT 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 801 CTTGAAAAGTCATTGCCGGAAGACCTTGTTAAAGAGATAATTGATAGACGTAAAGAGCTT 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="BOHK"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers" 133 c 183 g 252 t
                      BOHK Brassica oleracea genomic clone BOHKB84, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                haploid provided by Tom Osborn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 172.2; DB 12; Length
Pred. No. 7.9e-23;
); Mismatches 73; Indels
  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                 9712 Medical Center Drive, Rockville, MD
  DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Brassica oleracea"
  785 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:3712"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spernatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Spernatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

1 (Dases 1 to 455)

2 Anderson, O.D., Chao, S., Dubcovsky, J., Echenique, V., Han, P.S., Hsia C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L., Stamove, B. and Tong, J.C.

The structure and function of the expressed portion of the wheat genomes - Vegetative apex cDNA library from Triticum monococcum Unpublished (2001)

Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center

800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Vegetative shoot apex"
/dev_stage="Three weeks-old plants"
/dab_nost="E. coli XLOLR"
/note="Vector: Lambda pBk-CMV (Lambda Zap Express),
excised phagemid; Site_1: ECORI; Site_2: XhoI; The tissue,
total RNA, and poly(A) RNA were prepared, a cDNA library
total RNA, and the cDNA clones were in vivo excised at the
University of California, Davis (V. Echenique, B. Stamova
J. Dubcovsky). Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
                                                                                                                                                                                                             BE493178 455 bp mRNA linear EST 16-APR-2001
WHE0570_C11_F22ZE Triticum monococcum vegetative apex cDNA library
Triticum monococcum cDNA clone WHE0570_C11_F22, mRNA sequence.
      496 TITATITIGAAAATAGAGTGGCATTGGCACGGATGTTATITCCTCAGGAAGCCATGCTAGC 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     715 TTGCTAATATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGATGTAAAGAGATTATTG 774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="WHE0570_C11_F22"
/clone_lib="Triticum monococcum vegetative apex cDNA
library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: oandersn@pw.usda.gov
Sequence have been trinmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene T3 primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Triticum monococcum"
/cultivar="DV92"
/db_xref="taxon:4568"
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Pred. No. 1.4e-20;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                BE493178.1 GI:9659771
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                                                1433 AATGGAGATCGC 1444
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                                                                                               567
                                                                                             556 TATGGAAATAGC
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Best Local 3
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ORIGIN
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                                                                                                                                                              RESULT 15
BE493178
                                                                                                                                                                                                                                                                           ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="vector: Bluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the fact for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                        Tracheophyta;
                                     Spermatouty Viridiplantae: Streptophyta: Embryophyta: Tracheophy Spermatophyta: Magnoliophyta: eudioctyledons; core eudicots. Asteridae: euasterida I: Solanales; Solanaceae; Solanum. I (bases 1 to 667) S. Solanales; Solanaceae; Solanum. Van der Hoeven, R., Bezerides, J., Sun, H., Cho, J., Chiemingo, Bougri, O., Buell, C. R., Ronning, C., Tanksley, S. and Baker, B. Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             956 GGATCACACCAATCTAGATGATGCGTGTGCTCTTCATTTCGCTGTTGCATATTGCAATGT 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1016 GAAGACCGCAACAGATCTTTTAAAACTTGATCT---TGCCGATGTCAACCATAGGAATCC 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1133 TCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGAACCGCACTCAT 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1193 GATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATATCCCGGAGCAATGCAAGCA 1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1253 TTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGACAAAACGAGAACAAAT 1312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    896 GAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTGAAAGA 955
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                                                                                                                                                                                                                                         Contact: Cathy Rouning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tell 1-800-711-6195, email cdna@resgen.com
Seq primer: M13F-R.
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/oultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTS2BE"
/clone="cSTS2BE"
/fissue_type="Sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
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Spermatophyta; Magnoliophyta; endicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

[Cao, H., Glazebrook, J., Clarke, J.D., Volko, S. and Dong, X.
The Arabidopsis NPRI gene that controls systemic acquired
resistance encodes a novel protein containing ankyrin repeats
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Cao, H., Glazebrook, J., Clarke, J.D., Volko, S. and Dong, X.
Direct Submission
Submitted (30-OCT-1996) DCMB Group, Botany, Duke University, LSRC
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RPANDFMLEVLXAETER!PELITYORHILDVVDKVVIEDITULILKILANICGRACMK
LLDRCKEITVKSNNDWYSLERSLPEELVKEIIDRREELGLEVPRVKHIVSNYHKALDS
DDIEZVKLLIKEDHPRUDDACALHFAVAYCOVKTAPDLIKLDLADVNHRNPRGYTVLH
VAANKREPQLILISLIEKGASASAEATLEGRAAMIARQATMAVDCNNIPEGCKREIKGR
LCVBILEGEDKREQIPROVPPSFAVAADELKMTILDEHRVALAQRLFPTEAQAAMEI
AEMGGTGFIVYSLEDPRILGTKRISPGVKIAPFRILLEHGSRIKKAFSEDNLELGRS
RICTANICGDLAGGEDDTAEKRLCKOKKQRYMEIQETLKKAFSEDNLELGNS
SLITSTSSTSSKSTGGRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGTGCACCGGTGCATTTTGTCGGGAGGAGTCCGTTCTTTAAGAATTTGTTCTGCGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAAGGAGAAGAATAGTAGT--------AAGGTGGAATTGAAGGAGGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                              36;
                                                                                                                                  /gene="NPR1"
/note="ankyrin repeat-containing protein; gene
systemic acquired resistance; SAR"
                                                                                                                                                                                                                                                                                                                                                                                       Length 2104;
 NC 27708-1000, USA
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                          DB 8;
                                                                                                                                                                                                                                                                                                                                                                                       Score 578.4; DB 8;
Pred. No. 3.7e-138;
0; Mismatches 546;
                                   /organism="Arabidopsis thaliana"
/strain="ecotype Columbia"
/db_xref="taxon:3702"
                                                                                   /map="between GAP-B and m315"
1. .2104
Research Dr., Durham,
Location/Qualifiers
1. .2104
                                                                                                                                                                                                                                                                                                                                                       482 q
                                                                        /chromosome="I"
                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 26.6%;
Best Local Similarity 62.8%;
Matches 982; Conservative C
                                                                                                          /gene="NPR1"
93. .1874
                                                                                                                                                                                                                                                                                                                                                       431 C
  Building,
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AAGCATTCACTGAGGATAAAGAAGAATATGATAAGACTAACAACATCTCCTCATCTTGTT 1953 TTCTAAATAAGATCATGGATGCTGATGACTTGTCTGAGATAGCTTACATGGGGAATGATA 1833 AGGCCTTTAGTGAGGACAATTTGGAATTAGGAAATTCGTCCCTGACAGATTCGACTTCTT 1812 GCCTGGCTAAACTCCTTTTTCCAATGGAAGCTAAAGTTGCAATGGACATTGCTCAAGTTG 1596 CGGCAGAAGAGCGTCAACTGAAGAAGCAAAGGTACATGGAACTTCAAGAAATTCTGACTA ATGATGCATATGCTCTCCATTATGCTGTAGCGTATTGCGATGCAAAGACTACAGCAGAAC ATGTTGCAGCCATGAGGAAAGAGCCTAAAATTGTAGTGTCCCTTTTAACCAAAGGAGCTA GACCTTCTGATCTGACATCCGATGGAAGAAAGCACTTCAAATCGCCAAGAGGCTCACTA CTCTTCCTATGCAGCCGATGATTGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTG GGACAACAGTAGATTTGAACGAGGCTCCTTTCAAGATAAAAGAGGAGCACTTGAATCGGC 1714 ITAGAGCACTCTCTAGAACTGTAGAACTTGGAAAACGCTTCTTCCACGTTGTTCAGAAG GGCTTGTGGATTTCAGTAAGTCTCCGGAGGAAGGAAAATCTGCTTCGAATGATCGGTTAT GCATTGAGATTCTGGAGCAAGCAGAAGAAGAAGACCCTCTGCTAGGAGAAGCTTCTGTAT ATGGCACTTCTGAGTTCCCACTGGCTAGCATCG----GCAAAAAGATGGCTAATGCACAGA TGGATTCTGATGATGATTACTACAAATGTTGCTAAGAGAGGGGCATACTACCTAG TICIAGAICITGCACTTGCTGATATTAATCATCAAAATTCAAGGGGATACACGGTGCTGC TACAAGGGCCTGAAAGCAACGGTTTTCCTGATAAACATGTTAAGAGGATACATAGGGCAT TGGAGGTACCTAAAGTAA------AGAAACATGTCTCGAATGTACATAAGGCAC

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LCVEILEGEDKREQIPRDVPPSFAVAÅDELKWTLLDERNRVALAGRLEPTEAGAAMEI
AEMKGTCEFIVTSLEPDRLTGTKRTSPGVKIAPFRILEEHQSRLKALSKTVELGKRFF
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                 DDIELVKLLLKEDHTNLDDACALHFAVAYCNVKTATDLLKLDLADVNHRNPRGYTVLH
VAAMRKEPQLILSLLEKGASASEATLEGRTALMIAKQATMAVECNNIPEQCKHSLKGR
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                                                                                                                                                                                                                                                                                                                                                                                                CGGAGTTTGACTACTTCGCCGACGCTAAGCTTGTGGTTTCCGGCCCGTGTAAGGAAATTC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     697 IGGCIIGIAGGCCAGCIGIGGCAIICCIGGIIGAGGIIIIGIACACAICAIIIACCIIIC 756
                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 577 TGAAAGAGCATGAGGTGAGCTATGATGCTGTAATGAGTGTATTGGCTTATTTGTATAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTAAAGTTAGGCCTTCACCTAAAGATGTGTGTGTTTGTGTGGACAATGACTGCTCTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              631 TGGCTTGCCGGCCGGCGGTGGTTTCATGTTGGAGGTTCTCTATTTGGCTTTCATCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             751 TTATAGAGGACACATTGGTTATACTCAAGCTTGCTAATATATGTGGTAAAGCTTGTATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           937 ATAAAGCCTTGCCTCATGACATTGTAAAACAAATTACTGATTCACGAGCGGAACTTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        997 TACAAGGCCTGAAAGCAACGGTTTTCCTGATAAACATGTTAAGAGGATACATAGGGCAT
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                                                                                                                                                                                                                                                                                              Length 2154;
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                                                                                                                                                                                                                                                                                                                                               0; Mismatches 546;
                                                                                                                                                                                                                                                                                           Score 578.4; DB 8 Pred. No. 3.7e-138
                                                                                                                                                     SLTDSTSSTSKSTGGKRSNRKLSHRRR"
1941. .2154
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62.8%;
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2. (Dases I to 2154)
8. Koesema.E., Chen,H., Cheuk,R., Kim,C.J., Meyers,M.C., Shinn,P.,
8. Banh,J., Bowser.L., Carrinci,P., Dale,J.M., Goldsmith,A.D.,
8. Hayashizaki,Y., Ishida,J., Jiang,P.X., Jones,T., Kamiya,A.,
8. Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X.,
Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J.,
Pham,P.K., Quach,H.L., Sakurai,T., Satcul,M., Scuthwick,A.,
Tang,C.C., Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S.,
Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.
Direct Submission
8. Submitted (O8-AuG-2001) Salk Institute Genomic Analysis Laboratory
(SIGnAL), Plant Biology Laboratory, The Salk Institute for
8. Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
8. Road Studies (C. M.) For the Palk CA 1011a, CA 92037,
8. Road Studies (C. M.)
                                                                                                                                                                                                           Puckaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eucosids II; Brassicales; Brassicaceae; Arabidopsis.

Rosema, E., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Shinn, P., Banh, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Miranda, M., Nguyen, M., Ondernith, Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Ondera, C.S., Palm, C.J., Tang, C.C., Toriumi, M., Yamada, K., Yamanara, Y., Yu, G., Yau, Southwick, A., Shinn, C.Y., Shinozaki, K., Davis, R., Theologis, A. and Ecker, J.R., Yu, S., Yu, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Koesema,E., Chen,H., Dateuk,R., Kim,C.J., Meyers,M.C., Shinn, P., Banh,J. BowSer,L., Lam,B., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G., Onodera,C.S., Palm,C.J., Pham,P.X., Quach,H.L., Southwick,A., Tang,C.C., Toriuni,M., Yamada,K., Yamamura, Y., Yu,G., Yu,G., Yu,S., Tang,C.C., Toriuni,M., Yamada,K., Yamamura, Y., Yu,G., Yu,S., Davis,R.W., Theologis,A., and Ecker,J.R.
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AQULLSNSEESYEDSPDDFYSDAKLVLSDGREVSFHRCVLAARSSFFKSALAAAKKEK
DSNNTAAVKELKEIAKETSTSTSTGFESVYVLAAFVYSSRVRPPRGVSECADBNCCHVAC
RPAVDFMLEVLYLAAFFKIPELTFKYPELTLYCKHLLDVVDKVVIEDTLVILKLANICGKACM
LLDRCKEIIVKSNVDMVSLEKSLPEELVKEIIDRRKELGLEVPKVKKHVSNVHKALDS
                                     20-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN Genomic Sciences Center (GSC) members carried out the
                    ALUSU455 2154 bp mRNA linear PLN 20 Arabidopsis thaliana At1g64280/F15H21_6 mRNA, complete cds AY050455
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/db_xref="taxon:3702"
/chromosome="1"
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/protein_id="AAK91469.1"
/db_xref="G1:15215850"
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                  GGACAACAGTAGATTTGAACGAGGCTCCTTTCAAGATAAAAGAGGGGCACTTGAATCGGC 1713
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disease resistance
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Pred. No. 1.1e-130;
0; Mismatches 476;
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1 (bases 1 to 1597)
Uknes, S. Joseph, Hunt, M. Denise, Steiner, H. Altered forms of the NIMI gene conferring
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Sequence 9 from patent US 5986082.
AR087501
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Best Local Similarity 63.9%;
Matches 870; Conservative
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/tanslatton="MPFSAMRHLLDFLDKVEVDNLPLILSVANLCNKSCVKLFERCM
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VDGTLEFTLGSSTNPPLEITTVDLNDTSFKMKEEHLARMRALSKTVELGKRPFPRCSN
VMCTLEFTLGSSTNPPLEITTVDLNDTSFKMKKEEHLARMRALSKTVELGKRPFPRCSN
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VMCTLEFTLGSSTNPFLEITTVDLNDTSFKMKKEEHLARMRALSKTVELGKRPFPRCSN
VMCTLEFTLGSSTNPTLSSSTNFTTLTSSSSSST
        06-FEB-2002
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                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Wang, H.X., Salmeron, J.M., Willits, M.G. and Lawton, K.A.
Monocotyledonous plant genes and uses thereof
Monocotyledonous plant genes and uses thereof
Patent: WO 0166755-A 19 13-SEP-2001;
Syngenta Participations AG (CH)
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larity 67.0%; Pred. No. 4.7e-125;
Conservative 0; Mismatches 374;
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/note="unnamed protein product"
      DNA
                                                                                                                                                                                                                                                                /organism="Triticum aestivum"
/db_xref="taxon:4565"
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Uknes,S.Joseph., Hunt,M.Denise., Steiner,H.-Y. and Ryals,J.Andrew.
Altered forms of the NIMl gene conferring disease resistance in
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                      GAAGAAAAGCACTTCAAATCGCCAAGAGGCTCACTAGGCTTGTGGATTTCAGTAAGTCTC
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                                                                          TGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTGGCCTGGCTAAACTCCTTTTTCCAA
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                                             CTTTCCACCGGTGCGTTTTGTCACGAGAAGCTCTTTCTTCAAGAGCGCTTTAGCCGCCG
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LADVNHRNPRGYTVLHIAARRREPKIIVSLITKGARPADVTFDGRRAVQISKTITKQG
DYFGYTEEGRFSPFNDRLCIEILEGARREPGUGGASVSLAMAGESLERGRLIXLENRVA
LARIMFPMEARVAMDIAQVDGTLEFNIGSGANPPPERGRTTYDLNESFIKKEEHLAR
HTALSKYTVELGKRFFPRCSNVLDKINDDETDPVSLGRDTSAEKRRFHDLQDVLQKAF
HTALSKYTVELGKRFFPRGSSSTSTGLGAIRRR"

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/db_xref="GI:18616495"
/translation="GAFPPARAGGLLLLLLAELTNLFQRRLLDVLDKVEVDNLLLIL
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
CTITIGCAGIGGCGGCCGAIGAATIGAAGAIGACGCIGCICCATCTIGAAAAIAGAGTIG 1342
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                              GCCTGGCTAAACTCCTTTTTCCAATGGAAGCTAAAGTTGCAATGGACATTGCTCAAGTTG
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                                                                                         ATGGCACTTCTGAGTTCCCCACTGGCTAGCATCG---GCAAAAAAAGATGGCTAATGCACAGA
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Pred. No. 2.7e-121;
0; Mismatches 395;
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/db_xref="taxon:4530"
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1060 ATTCTGATGATGTTGAATTACTACAAATGTTGCTAAGAGGGGGCATACTACCCTAGATG
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                                                                                                                                                                                                                                                Length 1194;
      linear
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                                                                                                   1 (bases 1 to 1194)
Uknes, S. Joseph, Hunt, M. Denise, Steiner, H.
Altered forms of the NIM1 gene conferring
                                                                                                                                                                                                                                             Score 490; DB 6; I
Pred. No. 2.3e-115;
                                                                                                                                                                                                                                                                     Mismatches 410;
      DNA
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Patent: US 5986082-A 13 16-NOV-1999;
Sequence 13 from patent US 5986082. AR087506
                                                                                                                                                                                         /organism-"unknown"
227 c 294 g
                                                                                                                                                                    Location/Qualifiers
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                                         GI:10014269
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Best Local Similarity 64.5%;
Matches 771; Conservative
                                                                                          Unclassified.
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                                                               Unknown
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              DEFINITION
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linear PLN 26-JAN-2001
PAC clone:P0001B06.
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Eukaryota, Virialplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae, Oryza.
1 (bases 1 to 140304)
Sasaki, T. Matsumoto, T. and Yamamoto, K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone: P0001B06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sasaki,T., Matsumoto,T. and Yamamoto,K.

Direct Submission

Submitted (21-JUN-200) Takuji Sasaki, National Institute of
Agrobbological Resources, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 309-8602, Japan

(E-mail:tsasakiaabr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)

on Oct 19, 2000 this sequence Varsion replaced g1:8698575.
Genes were predicted from the integrated results of the following:
GENSCANI.0, BLASTN2.0, BLASTX2.0 as well as SplicePredictor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAGAAGAGCCCTCTGCTAGGAGAAGCTTCTGTATCTCTTGCTATGGCAGGCGATGATT 1500
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TTATTGTCAAGTCTAATGTTGATATCATAACCCTTGATAAAGCCTTGCCTCATGACATTG 960
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                 1141 CTGTAGCGTATTGCGATGCAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCTGATA
                                                                                                                                                                                                                                                  1952 GAAGAAAAGCAGTICAAATCTCAAAGAGACTCACAAAACATGGTGATTATTTTGGGAATA
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                                                                                                                  1021 TICCIGATAAACAIGITAAGAGGATACATAGGGCAIIGGAITCIGAIGAIGTIGAAITAC
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AP002537/c
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                                               Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
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Monocotyledonous plant genes and uses thereof
Patent: WO 0166755-A 113-SEP-2001;
Syngenta Participations AG (CH)
Location/Qualifiers
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/db_xref="taxon:4565"
/1396. .2163
2338. .2532
2533. .2933
2934. .3188
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Pred. No. 4.8e-90;
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AX351127
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69.9%;
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Matches 528; Conservative
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AX351127
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(October 1998 version). The genomic sequence was searched against (ftp://ncbi.nlm.nlm.gov/blast/db) and the CDNA sequence database at RGP. Protein homologies of the coding regions were searched against RGP. Protein homologies of the coding regions were searched against the identified CDNA sequences using BLASTP 2.0 with the corresponding DDBJ accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and 'like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from SPG to Ty of the PAC clone. This sequence of PQ001B06 clone has an overlap with P0671B11.

Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html Detailed information on overlap and assembly quality together with a savailable at http://rgp.dna.affrc.go.jp/GenomeSeq.html. Location of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
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GLLHRCAIGAAHNSLCRVLLHEVWEWBGEAAAAAAAAAAAEAAEDRALRGIWAVGLLCR
WQPQPQCSSKLTISCTPLH"
7047. 7694
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SSSSSSSSEEKEVSKDVAVETSVVVPSVVAASPDDEAAAVASGDGGDVIKHDDEAV
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AKPPGSSQAEWSVASNESLFSIHHGARPSGDLCGFYAGESRSHFDYFYDEAMAGAAG
DHTSDWKLATVAEGSPGGSARSDATDGGGGAAKQKAAIDFRRHESGSAGSSSNFSFAF
PWYAADDAIVIGGDDDVAEEEGLRRDVPSAEEGGGAAAGGVAGVGVRGDDAGGGAAAA
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/gene="P0001B06.4"
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/gene="P0001806.4"
/note="hypothetical protein
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/organism="Oryza sativa"
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join(2486. 2566,4
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FEATURES

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/translation-manabahaaasplrrrlphhrgrrllavaaalspeppappy
Trspppprkgyperkrubuletregiaptyrgkgycydogspyllcdcalpgerllar
Trspppprkgyperkrubuletregiaptyrgkgycydogspyllcdcalpgerllar
VRRIRRGAPABAAAAAAAAAAPCPLAADGGGCRAGSLAYAQIRHKHLOVRE
LLVWRGKPDPRKMESSEDALIKPIVPCDEIFRYRRKMEFSFGTKRWMGREWEEKDD
EVVKERWEGSTGLILAPTGFPLYTTGAPEVWNWTYSCYRPELLEPLYNNITTPEPVUS
IMNVNTSYGATSYGEBETTLAFGAPEVWNWTYSCYFPELLEPLYNNITTPEPVUS
IMNVNTSYGGRETTLILDFGGTTIGLTARRAKHVYGYEVVPBAIAARKNAKINGIS
NATFVQGDLNKINETFGKEFPKPDIIISDPNRFGMHWKLIKMLLEVKAPRIVYSCNP
AGRARDLDYLCHGYBEKDLEKGCYELKTVIPVDMFPHTPHIECICVLELC"

join (19026. 19092, 19440. 19762)

/gene="P0001806.6"
| Join (19026. 19092. 19440. 19762)
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join(22508. .22615,22741. .22836,22932. .22994,23274. .23351,
23844. .24652,24235. .24648,25397. .25480,25581. .25726,
26248. .26508,28585. .26766,26859. .27141,28140. .28334,
28526. .28741,28826. .28978,29068. .29265)
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                                                                                                                                                     /translation="MSADGGDPFDSLPAAIAADVLGRVADGADIAAYCLASRAFLAAS
YACSRVHLRAAALARRRSVALAGGGGGGPPGGSAIRAAAGNAASLLGPHLRSLELDAS
EGWGHPDDATWVEEGEFDEGGDLHLTAREAVVAWADTAAGNALREVDVADYWPOSCWR
                                                                                                                                                                                                                                                                                                                  LDDEDLNKLNECFPCLQILNLIGVGGLKDPKIHLHQLKTCHWEVSKNYPRSLTIRRPN.
VRLELKCVRPDMLILDTPSMFTLKLIYDKLGPNVQADGLVSLKNLRIESLDLKSLLQV
FASHNDITTLELELPTSTNKYELFEAVKPEYLLQLFAGISEVKLAPRFSCEMTHCLML
CTSNOFRSCLRRLLFPPLKVDPHLAPLFNNCAPSCEVTILFHADSSDDIRQAATSV
WTLRYPGIRWQWGTWN
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VEKGEDDGSGRSTCSPCAAYVSRCGLERTVLAAVQIRQLSEGSMLRRRRKRPGDWPLL
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RQVDATECALNSDLERGTVDLPESTANISTKIPDLPSQLKPEINMSRRSKRKSKSPCG
SKYVVCNGADNLQARRLQHCLSSESLRRWCTYEWFYSAVDYPWFMDNEFVNYLNFANL
SHLSRLTRSEWSTIRSSLGKPRRFSDHFLAABKDKLENYRKKVRQYYALLSEDSWDSL
                                                                                                                                                                                                                                                                            KAEALPSIWSTLVWSQIETSAIHAGHSLLKLRLKNAWLSVDGLKIMPNLTHLTLEFIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(14597. .14704,14802. .14932,15057. .15223,
15388. .15503,15664. .15819,16008. .16116,16591. .16700,
17245. .17430,17515. .18105))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(14597, .14704,14802, .14932,15057, .15223, 1538, .15503,15664, .15819,16008, .16116,16591, .16700, .17245, .17430,17515, .18105))
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GFVALVTGHHNVSDESKSHKGSDQTVRASGKVRKREATGQKEKEAPHAHRSYHERRTS
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GATNNELECSSHGSPGISESAKFVQGQTFLEAKGTGSLKKRRIEQSMEQGGTIKDEHK
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VNWLDNLPDDLKKRSFLSNNSHNRVEVEQIPKFTSKENWDHISGEAEPSKTMHITSDE
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23884. .24052.24235. .24018,23397. .25480,25581. .25726,
26248. .26508,26585. .26766,26859. .27141,28140. .28334,
28526. .28741,28826. .28978,29068. .29265)
to Arabidopsis thaliana chromosome 4, AT4g29420"
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similar to Arabidopsis thaliana chromosome 3, F22F7.18"
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Oryza sativa
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AP002746/c
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TITLE
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RTTPPAPTHRDNRKSLEAGTYHEVLDLKQLLDLADERHKVAYVSRSKRNSDSSSVSSM
SYSSSSTISTISTSASSGGASEPGLESKRRLLDWRRKSRDFDKRSSESLGQELDMKY
MDDDLAGSWETREFFSRDSFTKLFVPFFASTDQRDDSAGGESACTALVAVLAAALHA
NHPTHRPTRPELDALIRDGSSEWRRLCDDEAHMAAFPNRHFDLETVLAARARPIAVQHD
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                                                                                                                                                                                                                                                                                /translation="MWRVATVGDLPLGPTRAGAHREAEAAAKPARVVVVVVRPRDTAS
SAAARGESSTRVIDBSIVCEVBEGVGWTERRASPAAAAGRRRGGVRYGPTRLEGMP
SAAARGESSTRKVIDBSIVCEVBEGVGWTERRASPAAAAGRRRGGVRYGFBREGFRFGFBCGVBARFFF
DLDQPSAAAVAVKWPVSGFSILYGFORGGRGCNDVVKLEEIGTAMISLEECCWEWQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAFVGFFQPESFASLSGAMSFDDIWREIAAAAGGEPGRADVYIVSWNDHFFVLKVEGD
CYHVVDTLGERLFEGCDKAYMLRFDATSEMRSVSPPPSSPSPEBEVIVTGKECCREFI
QVETAVDÍERLSNKSTSGNCGPLQPLOSVDDNVRSRGLSEHRNGHNDELDSYITSFVQ
MSLAQAKQMVDEAMKEISENGKSSLEETGISNEATDCTGPEPESAANSELPRNLÍFNC
                                   IATLLAIKHFSEGRHPPPNIAGVLERACLMLRPSCAENLPIYNEIENFIAVIKNQILA
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32874, .33367,33459, .33519))
/gene="P0001B06.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55101 TCAAGCAGATTATTGATGCACGCCTAAGCCTCGGATTAATTTCACCAGAAAACAAGGGAT 55042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55281 TGCAGCGGCGTCTCCTTGATGTCCTTGATAAGGTTGAGGTAGATAACCTTCTATTGATCT 55222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1081 TACAAATGTTGCTAAGAGAGGGGCATACTACCTAGATGATGCATATGCTCTCCATTATG 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTAAAATTGTAGTGTCCCTTTTAACCAAAGGAGCTAGACCTTCTGATCTGACATCCGATG 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCCTGATAAACATGTTAAGAGGATACATAGGGCATTGGATTCTGATGATGATTAC 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGTAGCGTATTGCGATGCAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCTGATA 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGAAAAGCACTTCAAATCGCCAAGAGGCTCACTAGGCTTGTGGATTTCAGTAAGTCTC 1380
                                                                                                                                                                                   /note="contains ESTs AU098333(E40118),AU098332(E40118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATCTGTTGCAAACATTTGTGGTAAAGCATGCGAGAGATTGCTTTCAAGCTGCATTGAGA 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            781 TICAGAGACACCIACIGGATATICITGACAAAACIGCAGCAGACGATGTAAIGATGGTIT 840
                                                                         .30866,30967. .31395,31505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54861 Traatcaragaacccaagaggtraractgrictrcacattgctgcgaggggagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTATTGTCAAGTCTAATGTTGATATCATAACCCTTGATAAAGCCTTGCCTCATGACATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAAAACAAATTACTGATTCACGAGCGGAACTTGGTCTAÇAAGGGCCTGAAAGCAACGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRFLAAIPLREELEMERKGCADAPHRRLQIEFHFTVLKEEEDDOARR" complement(join(35488. .35671,36191. .36240))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 140304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 376.4; DB 8;
Pred. No. 4.5e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 276;
                                                                   complement(join(30030, .30866, 32874, .33367, 33459, .33519))
                                                                                                                                                                                                                                           /protein_id="BAB16855.1"
/db_xref="G1:10934077"
                                                                                                                                                                                                           unknown protein"
                                                           LVPSASSNARLPMYM"
                                                                                                                                                                                                                               /codon_start=1
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ILNYIPKPQSRKSSHITCKNRVKLYPWTVWVAVFADVASMSVPARGVGGVRWIRLGEA
ADDVVEBERLGDRGRRASVRVDELLPPFTTTCKYQLPSFTAVESNANNGARCNTTPLAS
ADDVVEBERLGDRGRRASVRVDELLPPFTTTCKYQLPSFTAVESNANNGARCNTTPLAS
NGDTVKWPEQGADNRELLPPCNKTSFFRDLSDRATPNNDTSGYQDSHSGHPWTTFPAC
SSVSVAIVRAAMAPRERLLFPCNTNTSSTRATPNNDTSGYQDSHSGHPWTTFPAC
SSVSVAIVRAAMAPRELLLSPSIDDWQMHFS"
31461. 314899
/ Anote="Fof11811.5"
31951. 34899
/ Gene="Pof71811.5"
31951. 34899
/ Gene="Pof71811.5"
/ Onte="contains EST AU078159(S0050)"
join(21560. .21603,21647. .21823,23060. .23299,23892. .23912,
24246. .24483,24832. .24987,27438. .27609,27873. .28087)
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NNSGPSVLDATEIFDKLRVAPDVYFKNIKKAGSMGASTALAMTKSLYPRIEIDAIDGF
ADRTSVEAALDLISNAQNAADKIASDVVDQFRNTDLQPSSNNSDDERTDSD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INAVQPDTPQYLRWSEIAIKEDRSDHPDRVUHPGRYPLVLDPVVRNYKLRRTLIDGGS
ALTILERAKTLDDMQIERSEBERSNAPHEUVIEDLSAFPLGGOTILLVPFGTRENFRTEN
ISFEVADFETAYHALIGRPALAKFMAVPHYTYMMMKNPGPRGVLSLRSDIKQBYDTCDF
ESCDMAQTRETASAREDIRLAAATASEGEVPATKTSKSGESEAKTNKIPLDPSNPTKT
                                                                                                                                                                                                                                                                                                                                                                                        ATAAVAGDRRGGGGGGGGGGRTPRRRRRTHHQFTVVVRRVITKSKCDLILVMAGND
LSFAETKKKRRRNLVCPHEEARGQQTDGPDVDTSEGASSLDRMIAGGVRVSWYSLRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MGSVSGIDDLVFPPGQTFRFGSLDFVTNNFGKISLLDSESDQSG
ENRISVPFGLPNAAESYFKTVSIELASNHSGGIASSPMSPDQDDEAYPPILMKLPDDL
AAVSITTASPSRRPRRKSASTPISPSFREVGVILQPLGTVSTDQLDGYYSSPTVDSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QYTKTTRKNSDDEQSTSRKKDDGDTPVGFQDHRKELNHIFGGPLAYESKRKQKLTERE
                                                                                                                                                                                                                                                                                                                                                    /translation="MYHVILARYRMILTRVGAPRHAQSPPAAVPCRRGWRRQGQRTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="probably inactive due to frameshift and stop codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative gypsy-type retrotransposon RIRE2 orf5"
/protein_id="BAB12691.1"
/db_xref="GI:9988425"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/product="putative gypsy-type retrotransposon RIRB2 orf4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pseudogene, gypsy-type retrotransposon RIRE2 GAG-POL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative gypsy-type retrotransposon RIRE2 GAG-POL precursor"
                                                                                                                                  /note="contains EST AU058063(E20266)
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="P06/1B11.8"
/gene="P06/1B11.8"
/gene="rof"
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/gene="P0671B11.7"
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/codon et=="
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/gene="P0671B11.7"
                                                                                                                                                                                                                                                      /protein_id="BAB12689.1"
/db_xref="GI:9988423"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAB12690.1"
/db_xref="G1:9988424"
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/gene="P0671B11.6"
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                                                                                     /gene="P0671B11.4"
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/ Protein_d="60" analymy TPDIAETACDAIQYVGKNDSFALSQGRTVAGESWRW
/ Lranslation="maykwy TPDIAETACDAIQYVGKNDSFALSQGRTVAGESWRW
/ Lranslation="maykwy TPDIAETACDAIQYVGKNDSFALSQGRTVAGESWRW
| HEETHIVLISINESCOBAGREEGAPLVIAGLSVTVYPAAACCECASGNDADSFRR
| HEETHIVLISINESCOBAGREEGAPLVIAGLSVTVYPAAACCECASGNDADSFRR
| PTYPSMYPQVSGLIPWYGGLIPRYBPYSWYDSIPKRSIPWYGAAPPRRRRRRBAE
| VYPLWLTALVGVRGSTRAAPAASTSSMAAKWALKLLEHTYCAGDAGYVLEDVPHL
| TOYLPELPTYPRLQOPRAYSVYRIPLFHSTSTTAGTKRLFHTTCAGDAGYVLEDVPHL
| TOYLPELPTYPRRAGPRAYSWYRIPLFHSTTAGTKRLFHTTCAGGLCFGLNTVIREL
| VGGLYDWYGYTSWYGIEGGYKGFYSRWYALIPKSVNDIHKRGGTVLGTSRGGHDTGK
| VDDSIRNGGINVYYIIGGGGTWGGASVIFQPURRGLKCSVVGVPKTIDNDIQVIDKS
| FGFDTAVEBAQPRAINAFBAESAENGIGVVKLMGRNGGFTAMYATLASRDVDCCLIP
| ESPFILEGRGGLLEFIERRLKDNGHWYIVVAEGAGODLIAKSMNFVDTQDASGNKLLLL
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Joinf(21560. .21603.21647. .21823,23060. .23299,23892. .23912,24246. .244483,24832. .24987,27438. .27609,27873. .28087)
                                                                                                                             .6919,
.8231,
                                                                                                                                                                                                     8354. 8572)

gene="P0671B11.1"

Join (2314. 2477, 3897. .4069, 4075. .4227, 4366. .4489,

5212. .5449, 5890. .5936, 5988. .6115, 6223. .6423, 6713. .6919,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKDLISQMLVKNSAHRLPLHKLLEHPWIYQNADPSGYYRG"

complement(join(17576..18104,18181..18310,18411..18546))
/gene="P0671811.3"

complement(join(17576..18104,18181..18310,18411..18546))
/gene="P0671811.3"

/note="contains ESTs AU082307(E0784),"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRISPPRRCGRSSPPLSLLPPHGDRHRVALRGGEVWALGFYCSIRHYEGFNASPHSQ
EVERWYLSDPDIGKPLGRGREGHVYLAREKRSNH IVALKVLFKSQLKGGSQVEHQLRRE
VELOSHLRHPNILRLYGYFYPTRVYLILEFYALKGELYKELGYGKREGSREKSATYIASL
AHALIYLHGKHVIHPDIKPRNLLIGSQGELKIADFGWSVHTFNRRFMCGTLDYLPPE
MVEKTEHDYHVDIWSLGILCYEFLYGVPPFEAKEHSETYRRIVKVDLKFPLKPFVSPA
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AGYTGFTVAPVNGRHAYIPFYRITEKQNKVVITDRMWARVLCSTNQPCFLSHEDVEHL
KHDDDEHHLHNTQLLEGESSPVKDSSKCNGTAAPV"
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NDVKNHWNTKLKRRLAAAAACTPLLPLPAPPPLAATHTSPSSSLLLLPPLAVPTVKTE
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LVAHAMSAISRPSIILGAHTVTTNGSSARTHEAERNSTVERSTHVLKAASSPKSPKSP
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                                                                       join(2314. .2477,3897. .4069,4075. .4227,4366. .4489,5212. .5449,5890. .5936,5989. .6115,6223. .6423,6713.
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/note="contains ESTs C22394(C30013),C22393(C30013)"
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/protein_id="BaB12688.1"
/db_xref="G1:9988422"
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/gene="P0671B11.1"
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AU068014(C11507),C28532(C61484),AU090544(C61415)"
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phosphofructo-1-kinase"
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and Ryals, J. Andrew. disease resistance
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                                                                                                                                                                                                                                                                                   0; Mismatches 392;
                                                                                                                                                                                                                                Score 326.8; DB Pred. No. 2.7e-73
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Patent: US 5986082-A 1 16-NOV-1999,
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                                                                                           Location/Qualifiers
1. .5655
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ALQLLSNSFESVFDSPDDFYSDAKLVLSDGREVSFHRCVLSARSSFFKSALAAAKKEK
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Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Wagnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 5655)

Ryals,J., Weymann,K., Lawton,K., Friedrich,L., Ellis,D.,

Steiner,H.-Y., Johnson,J., Delaney,T.P., Jesse,T., Vos,P. and
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Steiner,H.-Y., Johnson,J., Delaney,T.P., Jesse,T., Vos,P.
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/db_xref="GI:1916912"
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DLDEVKKLLLKEDHTALDDAGALFRAYAYCNYTATDLIKLDJADVNHRNPRGYTVLH
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AEMKGTCEF TYTSLEEPRLICTRYRSPGVK TAPFRILEBHQSRLKALSKTVELGRRF
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Genes with

3787

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/product="hypothetical protein; 887-1915"
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RNDSPYFPGYPESPDLAGNPGSPDFSGNBQPSFRNNGGSPERFBNNGGAPIIRNPG
RNBDSPYFPGYPESPDLAGNPGSPDFSGNBQPPGFRNNGGAPIIRNPG
PTLGDGTANPGRGYGNRVGPTMEIESKMELAGRVKVLHVFTHHVVAKSDCRVTVSIAD
GSVLGFHC"
                   similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (seam Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/Repeatmasker.html).
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a
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putative non-autonomous DNA transposon - a consensus.
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensus.
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1
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/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 96887)
Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.J., M.W.D., Malti,R., Ronning,C.M., Koo,H., Fujil,C.T., Utterback,T.R., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana chromosome 1 BAC F15H21 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CGR-081.mit.edu/GBNSCAN.html), GeneMarkHmM (Mark Borodovsky, http://Genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant of GlimmerA, see Mihaela Pertea, http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html, and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLN 19-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9712
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                                                                                                                                                                                                                          1278 CTTTTAACCAAAGGAGCTAGACCTTCTGATCTGACATCCGATGGAAGAAAAGCACTTCAA 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC066689 96887 bp DNA linear PLN 19-JAN
Arabidopsis thaliana chromosome 1 BAC F15H21 genomic sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (25-APR-2000) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA, xlin@tigr.org 3 (bases 1 to 96887)
   1458 CTAGGAGAAGCTTCTGTATCTCTTGCTATGGCAGGCGATGATTTGCGTATGAAGCTGTTA
                                                                                                 1218 AGGGGATACACGGTGCTGCATGTTGCAGCCATGAGAAAAAGAGCCTAAAATTGTAGTGTCC
                                                                                                                               3967 ATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATATCCCGGAGCAATGCAAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC066689.5 GI:12323462
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Lin, X, and Kaul, S.
Direct Submission
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AC066689
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

AUTHORS TITLE

JOURNAL

COMMENT

JOURNAL REFERENCE

TITLE

JOURNAL AUTHORS REFERENCE TITLE

DEFINITION

ACCESSION

RESULT 15 AC066689

consensus."

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/traislation="MDEVSPYTAIKNLKPFKTSWCIOVKILHAWNHYTKGSGMSYEMM
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REDNMFAIOGALKPFSVAKFRQOLYTVUTENENNRYNIMELRYIKNNOPOFRSSNK
ESIONASNSGNNDLENENGAWYTIEFOKRGLPHAHILLEMHPTSKLSTAEDTDKYTTAEI
PDKKKKPELYAVVKDCMIHGPCGVGHPNSPCMENGKCKKYFPKSYSDTKVDNDGFPV
                                                                                                                                                                                                                                                                                                                                                                                                                        89099 AGACGTAAAAGTTGGAGTTGGAGGTACCTAAAGTAAAG------AAACATGTC 89146
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                                                                                                                                                                                                                                                                                                                                                                                          415 CGGAGTTTGACTACTTCGCCGACGCTAAGCTTGTGGTTTCCGGCCCGTGTAAGGAAATTC 474
                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88859 CACATTCATGAATATGTTCTTACTTGAGTACTTGTATTTGTATTTCAGAGGCACTTATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----AAGGTGGAATTGAAGGAGGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                577 IGAAAGAGCAIGAGGIGAGCIAIGAIGCIGIAAAIGAGIGIATIGGCIITAIIIGIAAIAGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTAAAGTTAGGCCTTCACCTAAAGATGTGTGTGTTTGTGTGGACAATGACTGCTCTCATG
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                                                                                                                                                                                                                                                                                                                                               112;
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                                                                                                                                                                                                                                                                                                  Length
                                                                        /product="unknown protein; 11471-16325"
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                                                                                                                                                                                                                                                                                           Score 326.8; DB 8;
Pred. No. 2.8e-73;
0; Mismatches 392;
     15418. .16325)
/gene="F15H21.18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   535 AAAAGGAGAAGAATAGTAGT----
                                                                                                                                                                                                                                                                                           15.0%;
58.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(6810. .6979,7311. .7400,7552. .7605,7688. .7759,7853. .7940,8028. .8095,8180. .8287,8409. .8792,9058. .9106,9145. .9224,9310. .9387,9478. .9629,9686. .>10294))
complement(6810. .10294)
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12686. .12786,13367. .13702,13835. .13925,14904. .15298,
                                                                                                                                                                                                                                                          /rpt_family="SIMPLEGUY1(SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensus." complement(join(<4109. .4202,4301. .4392,4524. .4606,4711. .4789,5171. .5398,5484. .5585,5691. .5826,6091. .6140,6390. .>6572)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to GI:3021357 from [Cyamopsis
tetragonoloba] (Plant Sci. 142, 147-154 (1999))"
complement(join(4109. .4202.4301. .4392,4524. .4606,
4711. .4789,5171. .5398,5484. .5585,5691. .5826,6091. .6140,
6390. .6572)
/gene="F15H21.11"
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LKIYGTDYTTKDGTGVRDYIHVVDLADGHICALQKLDDTEIGCEVYNLGTGKGTTVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MSLRVVSSVFSGINRIPNLHETHTLLRSHVFSFFFKPANIGSIR
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IVELEDCRSIISAAVSRGNVDLALSIFYTMRASFDLGTLISTLLLTQSGSDNDRWSWS
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KDGRESILLRPPSKDGDKILQPSFLIFLLALIATGAABASVIDSLEQLLSVATYTSL
AIGATLPERTVDVYGIXQQLLSQCDVVLQRR HBLKENVEKWMLARMCQLSNKTIAN
GEPAYRTRRTRVKKVRESLENSIKGKIDLIDSYARISSMIEIEVEMDSDVLAABAVNA
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NNNLTATITLLEVMAAHGCKKLVFSSSATVYGWPKEVPCTEESPLSGMSPYGRTKLFI
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                                                                                                                                                        complement(3384, .3459)
/rpt_family-"SIMPLEGUY1 SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensus.complement(3385, .3487)
                                                                        - a consensus
                                                                                                                                              - a consensus
     - a consensus
                    complement(3384. .3494)

TrpL_family="SIMPLEGUYI SIMPLEGUYI is a putative non-autonomous DNA transposon - a consensu complement(3384. .3457)
                                                                                                         /rpt_family="SIMPLEGUY1|SIMPLEGUY1 SIMPLEGUY1 putative non-autonomous DNA transposon - a concomplement(3384. .3459)
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DNA transposon
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/protein_id="AAG51706.1"
/db_xref="GI:12323467"
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/product="UDP-galactose 4
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complement(10465. .1
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/gene="F15H21.18"
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Search completed: October 8, 2002, 00:43:29 Job time : 3175.43 secs

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Perfect score:
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N_Geneseq_032802;*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Nicotiana glutinos N. tabacum NIM ho L. esculentum NIMI B. vulgaris NIMI h N. tabacum NIMI ho Arabidopsis thalia Arabidopsis thalia A. thaliana NIM-1 A. thaliana NIM-1
SUMMARIES	AAV16852 AAA97190 AAA97191 AAA97229 AAA97211 AAA97211 AAV16851 AAV46274 AAV46274
DB	19 21 21 21 21 21 19 19
Length	2172 1767 1731 2299 659 2024 2104 2011
% Query e Match Length DB	100.0 81.4 63.6 36.0 28.6 26.8 26.6 26.6
Score	2172 1767 1380.4 781.2 620.6 581.6 578.4 576.8
Result No.	H G B A G D A B D D D

97US-0046769. 96US-0023851. 97US-0035166.

16-MAY-1997; 09-AUG-1996; 10-JAN-1997;

97WO-US13994.

19-FEB-1998. 08-AUG-1997;

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	1 0	527.6	24.3	1608	77	AAH43384	ဗ္ဗ
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O	34	326.8	15.0	9919	16	AAV43658	A. thallana non-in
ပ	35	326.8	15.0	9919	13	AAV04631	Arabidopsis thalia
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	37	317	4	2368	22	AAC84340	Rice Nph1 cDNA seq
	38	316.2	14.6	786	19	AAV46279	NIN PU
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	40	315.4	14.5	2069	21	AAA61048	Rice putative nega
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KK	NPR1 myco	gene; a	cqui	red resistance; 1; insects; nem	tand	disease; plant atodes; viruses;	<pre>pathogens; bacteria; viroids;</pre>
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os N	Nicoti	ana	glutinosa	a.			
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                                                                                                                    The sequence is that of a homologue of the acquired resistance gene NPRI. It may be used in the production of transpenic cells which can produce the encoded acquired resistance protein. Such transpenic plant cells are useful in the production of plants having an increased level of resistance against disease caused by plant pathogens, e.g. bacteria, mycoplasmas, fungi, insects, nematodes, viruses, and viroids.
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             ACTIGICTGAGATAGCTTACATGGGGAATGATACGGCAGAGGGGGGTCAACTGAAGAAGC
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                                                                 ATGATAAGACTAACAACATCTCCTCATCTTGTTCCTCTACATCTAAGGGAGTAGATAAGC
                                                                                           Novel plant genes for enhancing systemic acquired resistance gene expression and broad spectrum disease resistance in plants, are homologues of Arabidopsis NIM1 gene -
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and their coding sequences from Arabidopsis thaliana, Brassica napus.

Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus annuus and Solanum tuberosum. NIM1 is one of the proteins involved in the signal transduction cascade leading to systemic acquired resistance (SAR) in plants. This gives the plants an increased resistance to disease. The gene and protein can be used to produce transgenic plants resistant to diseases caused by viruses, such as tobacco or cucumber mosaic virus, ringspot virus, pelargonium leaf curl virus, red clover mottle virus, remato bushy stunt virus, fungi, including Phythophthora parasitica and Peronospora tabacina, bacteria such as Pseudomonas syringae and Peabaci, insects, including aphids and lepidoptera and nematodes such as Meloidogyne incognita. In particular they can be used against disease
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present invention is concerned with the isolation of NIM1 homologues
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The present invention is concerned with the isolation of NIMI homologues and their coding sequences from Arabidopsis thaliana, Brassica napus, Micotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus annuus and Solanum tuberosum. NIMI is one off the proteins involved in the signal transduction cascade leading to systemic acquired resistance (SAR) in plants. This gives the plants an increased resistance to disease. The gene and protein can be used to produce transgenic plants resistant to diseases caused by viruses, such as tobacco or cucumber mosaic virus, ringspot virus, pelargonium leaf curl virus, red clover mottle virus, remato bushy stunt virus, fungi, including Phythophthora parasitica and Peronospora tabacina, bacteria such as Pseudomonas syringae and P. tabaci, insects, including aphids and lepidoptera and nematodes such as Meloidogyne incognita. In particular they can be used against disease
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                                                                                                                    disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
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                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                          AGACTAACAACATCTCCTCATCTTGTTCCTCTACATCTAAGGGAGTAGATAAGCCCAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                   Systemic acquired resistance; SAR; signal transduction cascade; disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;
                                                                                                    AGATAAAAGAGGAGCACTTGAATCGGCTTAGAGCACTCTTGGAACTGTAGAACTTGGAA
                                                                                                              AACGCTTCTTTCCACGTTGTTCAGAAGTTCTAAATAAGATCATGGATGCTGATGACTTGT
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                           CTAAAGTTGCAATGGACATTGCTCAAGTTGATGGCACTTCTGAGTTCCCACTGGCTAGCA
                                                                 TCGGCAAAAAGATGCCTAAATGCACAGAGGACAACAGTAGATTTGAACGAGGCTCCTTTCA
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
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expression and broad spectrum disease resistance in plants, are homologues of Arabidopsis NIMI gene

English. Claim 3; Page 127-130; 152pp;

The present invention is concerned with the isolation of NIMI homologues and their coding sequences from Arabidopsis thaliana, Brassica napus, Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus annuus and Solanum tuberosum. NIMI is one of the proteins involved in the signal transduction cascade leading to systemic acquired resistance (SAR) in plants. This gives the plants an increased resistance to disease. The gene and protein can be used to produce transgenic plants resistant to diseases caused by viruses, such as tobacco or cucumber mosaic virus, ringspot virus, pelargonium leaf curl virus, red clover mottle virus, tomato bushy stunt virus, fungi, including Phythophthora parasitica and Peronospora tabacina, bacteria such as Pseudomonas syringae and P. tabaci, including aphids and lepidoptera and nematodes such as Mellidogyne incognita. In particular they can be used against disease organisms of maize.

Sequence 2299 BP; 644 A; 483 C; 510 G; 662 T; 0 other;

4; ATAGTAGGACTGCGTTTTCTGATTCGAATGACATCAGCGGAAGCAGTAGTATATGCTGCA 306 203 263 408 468 383 528 443 503 627 563 687 747 683 807 867 803 CATGCGAGAGATTGCTTTCAAGCTGCATTGAGATTATTGTCAAGTCTAATGTTGATATCA 927 354 Gaps CTTCGAAACGAGAAGGAAGGAGGAGGATAAAGAGAGAGTGAAGCTTGAGCTTA 504 AGGATTTAGCTGGTGATTTTGAGGTTGGATTTGATTCGGTTGTTGCGGTTTTAGGTTATT **ACAAAACTGCAGCAGACGATGTAATGATGGTTTTATCTGTTGCAAACATTTGTGGTAAAG** ATTOTOGGCACCGCTTTCTCCGATTCCAACGACATCAGCAATGGCAGTAGCATCTGCTGCG TCGGCGGCGCCATGACTGAATTTTCTCGCCGGAGA------CTTCGCCGGCGG ACCCCCCCCCTCTCCCCCCTCTCTCAAAACCTCGACTCCCTTTTCCAACCCTCGCTTT **AAATTCCGGTGCACCGGTGCATTTTGTCGGCGAGGAGTCCGTTCTTTAAGAATTTGTTCT** AAGTCGCCGTTCATCGGTGTGTTCTCTCGTCGGAGCTCGTTCTTTCGGTCCGCTTTTG ------ATGAGGTGAGCTATGATGCTGTAATGAGGTGTATTGCTTATT TGTATAGTGGCAAAGTTAGGAATTTGCCTAGAGGAATTTGTGTGTTGGTTTGAGGGATT GCTCTCATGTGGCTTGTAGGCCAGCTGTGGCATTCCTGGTTGAGGTTTTGTACACATCAT TTACCTTTCAGATCTCTGAATTGGTTGACAAGTTTCAGAGACACCTACTGGATATTCTTG ACAAGATIGCACCAGATGACGITCTAGTAGTGTTATCTGTCGCTGAGATGTGTGGAAATG ---GT CTTTGCCGGAGTTTGACTACTTCGCCGACGCTAAGCTTGTGGTTTCCGGCCCGTGTAAGG 48; Score 781.2; DB 21; Length Pred. No. 3.1e-201; 0; Mismatches 528; Indels 36.0%; ilarity 67.3%; Conservative Local Similarity Best Local Sim! Matches 1186; Match 144 247 744 898 264 324 469 384 444 564 624 748 307 204 355 409 586 628 QQ 셤 g ò a ò QQ ç 셤 ò g ò Q ò g ö g ò g δ à ò

1407 1467 1827 AAGGAGCTAGACCTTCTGATCTGACATCCGATGGAAGAAAGCACTTCAAATCGCCAAGA 1347 AACTTGGTCTACAAGGGCCTGAAAGCAACGGTTTTCCTGATAAACATGTTAAGAGGATAC CTCAAGTTGATGGCACTTCTGAGTTCCCACTGGCTAGCATCGGCAAAAAGATGGCTAATG CACAGAGGACAACAGTAGATTTGAACGAGGCTCCTTTCAAGATAAAAGAGGAGCACTTGA ATCGGCTTAGAGCACTCTTAGAACTGTAGAACTTGGAAAACGCTTCTTTCCACGTTGTT CAGAAGTTCTAAATAAGATCATGGATGCTGATGACTTGTCTGAGATAGCTTACATGGGGA ATGATACGGCAGAAGAGCGTCAACTGAAGAAGCAAAGGTACATGGAACTTCAAGAAATTC 1755 AAGATACTCCAGAGGAACGGCAAAGGAAGAGAAACGATACCTTGAACTGCAAGACGCTT TGACTAAAGCATTCACTGAGGATAAAGAAGAATATGATAAGACTAACAACATCTCCTCAT ATAGGGCATTGGATTCTGATGATGTTGAATTACTACAAATGTTGCTAAGAGGGGGCATA CGGTGCTGCATGTTGCAGCCATGAGGAAAGAGCCTAAAATTGTAGTGTCCCTTTTAACCA CTTCTGTATCTCTTGCTATGGCAGGCGATGATTTGCGTATGAAGCTGTTATACCTTGAAA ATAGAGTTGGCCTGGCTAAACTCCTTTTTCCAATGGAAGCTAAAGTTGCAATGGACATTG CTACCCTAGATGATGCATATGCTCTCCATTATGCTGTAGCGTATTGCGATGCAAAGACTA TAACCCTTGATAAAGCCTTGCCTCATGACATTGTAAAACAAATTACTGATTCACGAGCGG CCACCATTGATAAATCCTTGCCGCAGAATGTTGTGAAACAGATAATCGACACGCGAAAGG CAGCAGAACTTCTAGATCTTGCACTTGCTGATATTAATCATCAAAATTCAAGGGGATACA CITGIICCICIACAICIAAGGG 1969 1695 1888 1815 1948 1648 1708 1635 1828 1048 1108 1044 1168 1104 1228 1164 1288 1224 1348 1284 1408 1344 1468 1404 1528 1464 1588 1524 1575 1768 804 924 988 984 q QQ δλ qq οy Ω δý q QY Ω Ω QQ οŽ g δy ρp Ω g οy Dp δλ qq ŏ g qq óλ Q Οy δλ ò g ò g δy δy

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RESULT 5 AAA9721

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1311 ACATCCGATGGAAGAAAGCACTTCAAATCGCCAAGAGGCTCACTAGGCTTGTGGATTTC 1370
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                                                         1011 AGCAACGGTTTTCCTGATAAACATGTTAAGAGGATACATAGGGCATTGGATTCTGATGAT
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01-APR-1999;
06-APR-1999;
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16-APR-1999;
19-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       951 CATGACATTGTAAAACAAATTACTGATTCACGAGCGGAACTTGGTCTACAAGGGCCTGAA 1010
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                                                                                                                                                                                                                              Systemic acquired resistance; SAR; signal transduction cascade; disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel plant genes for enhancing systemic acquired resistance gene expression and broad spectrum disease resistance in plants, are homologues of Arabidopsis NIM1 gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 659 BP; 200 A; 124 C; 153 G; 182 T; 0 other;
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Pred. No. 5.8e-158;
0; Mismatches 24;
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                                                                                                                                                                                                                                                                                                                                                                                          /product= "NIM1 homologue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 102-103; 152pp; English.
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1875 CGTCGTCGTCGACTCCAATGGG 1896
                                                                                       BP.
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ilarity 96.4%;
Conservative
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99US-0130449. 99US-0130449. 99US-0130449. 99US-0130891. 99US-0131449. 99US-0132407. 99US-0132484. 99US-0132486. 99US-0132487. 99US-0132487. 99US-0134218. 99US-0134219. 99US-0134219. 99US-0134219. 99US-0134219. 99US-013421. 99US-013422. 99US-013422. 99US-013422. 99US-013422. 99US-013422. 99US-013422. 99US-013423. 99US-013423. 99US-0134454. 99US-0134454. 99US-0139457. 99US-0139457. 99US-0139457. 99US-0139458. 99US-0139458. 99US-0139458. 99US-0139458. 99US-0139458. 99US-0139458. 99US-0139462. 99US-0139463. 99US-0139463. 99US-0139463. 99US-0139463. 99US-0139463. 99US-0139483. 99US-0139789. 99US-0139789.	900S-0142977 900S-0143542 900S-0144602 900S-0144086 900S-0144086 900S-0144331 900S-0144331 900S-0144333
PR 21-APR-1999; PR 23-APR-1999; PR 23-APR-1999; PR 23-APR-1999; PR 30-APR-1999; PR 04-MAY-1999; PR 06-MAY-1999; PR 11-MAY-1999; PR 11-MAY-1999; PR 11-MAY-1999; PR 11-MAY-1999; PR 12-MAY-1999; PR 21-MAY-1999; PR 21-MAY-1999	12 - 70L - 1999 13 - 70L - 1999 14 - 70L - 1999 15 - 70L - 1999 16 - 70L - 1999 19 - 70L - 1999

UUS-0144352 UUS-01446352 UUS-0144884 UUS-0145086 UUS-0145086 UUS-0145086 UUS-0145087 UUS-0145087 UUS-0145192 UUS-0145192 UUS-0145145 UUS-0145145 UUS-0145145 UUS-0145145 UUS-0145214	005-0145918 005-0145918 005-0145919 005-0146389 005-0146389 005-0147302 005-0147302 005-0147302 005-0147302 005-0147403 005-0147416 005-0147416 005-0147416 005-0147416 005-0148319 005-0148319 005-0148319 005-0148319 005-0148319 005-0148319 005-0148319 005-0148319 005-0148319 005-0148319	9908-0149930. 9908-0149930. 9908-0150566. 9908-0151066. 9908-0151066. 9908-0151303. 9908-0151303. 9908-01513130. 9908-01513130. 9908-0152363. 9908-0152363. 9908-0152486. 9908-0154486. 9908-0154139. 9908-0155139. 9908-0155139. 9908-0155139. 9908-0155139. 9908-0155139. 9908-0155139. 9908-0157865. 9908-0157865. 9908-0157865.
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                                                         ATGTTGCAGCCATGAGGAAAGAGCCTAAAATTGTAGTGTCCCTTTTAACCAAAGGAGCTA
                                                                                             TTCTAGATCTTGCACTTGCTGATATTAATCATCAAAATTCAAGGGGATACACGGTGCTGC
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                                                                                                                                                                                                                                                                                                              Length 2024;
                                                                                                                                                                                                                                                                                                             DB 21;
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Pred. No. 3.7e-147;
0; Mismatches 544;
990S-0159331.
990S-0159637.
990S-0159538.
990S-0160741.
990S-0160767.
990S-0160776.
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62.9%;
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TGGCTTGCCGGCCGGCGGTGGATTTCATGTTGGAGGTTCTCTATTTGGCTTTCATCTTCA
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                                                                                                                                                                                                                                                                                                                                                             The sequence is that of the acquired resistance gene NPRI. It may be used in the production of transgenic cells which can produce the enco acquired resistance protein. Such transgenic plants cells are useful in the production of plants having an increased level of resistance against disease caused by plant pathogens, e.g. bacteria, mycoplasmas, fungi, insects, nematodes, viruses, and viroids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGAGITIGACTACTTCGCCGACGCTAAGCTTGTGGTTTCCGGCCCGTGTAAGGAAATTC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
           pathogens; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGTGCACCGGTGCATTTTGTCGCGAGGAGTCCGTTCTTTAAGAATTTGTTCTGCGGTA
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                                                                                                                                                                                                                                                                                                       New isolated plant acquired resistance polypeptide gene - useful for, e.g. producing plants with increased resistance to pathogens such as bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 19; Length 2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
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      ..... yewe; acquired resistance; disease; plant pathogens mycoplasma; fungi; insects; nematodes; viruses; virolds; transgenic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2104 BP; 606 A; 431 C; 482 G; 585 T; 0 other;
                                                                                        /*tag= a
/product= acquired resistance protein
/note= NPR1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 578.4; DB 19;
Pred. No. 2.8e-146;
0; Mismatches 546;
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                                                                    Location/Qualifiers
93..1874
                                                                                                                                                                                                                                                                                                                                                Claim 9; Fig 5; 127pp; English.
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62.8%;
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                                                                                                                                                                                                                              HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                   Arabidopsis thaliana
                                                                                                                                                                                                                                                          Cao H,
                                                                                                                                                                                                                                                                            WPI; 1998-159458/14
P-PSDB; AAW46940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                              (GEHO ) GEN HOSPIT
(UYDU-) UNIV DUKE.
                                                                                                                                                                    08-AUG-1997;
                                                                                                                               WO9806748-A1
                                                                                                                                                                                       16-MAY-1997;
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                                                                                                                                                                                                                                                          Ausubel FM,
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Matches 982;
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GACCTTCTGATCTGACATCCGATGGAAGAAAAGCACTTCAAAATCGCCAAGAGGCTCACTA 1356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGACAACAGGTAGATTTGAACGAGGCTCCTTTCAAGATAAAAGAGGAGCACTTGAATCGGC 1713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCTTGTGGATTTCAGTAAGTCTCCGGAGGAAAGGAAAATCTGCTTCGAATGATCGGTTAT 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1774 ITCIAAATAAGATCATGGATGCTGATGACTTGTCTGAGATAGCTTACATGGGGAATGATA 1833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTTAAAACTTGATCTTGCCGATGTCAACCATAGGAATCCGAGGGGATATACGGTGCTTC 1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1153 GIGCATCAGAAGCAACTITGGAAGGTAGAACCGCACTCATGATCGCAAAACAAGCCACTA 1212
                                                                                                                                                                                                                                                                                                                                                                                            TACAAGGGCCTGAAAGCAACGGTTTTCCTGATAAACATGTTAAGAGGATACATAGGGCAT 1056
                                                                                                                                                                                                                                                                                           ATAAAGCCTTGCCTCATGACATTGTAAAACAAATTACTGATTCACGAGCGGAACTTGGTC 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACTTGCTCAACGTCTTTTTCCAACGGAAGCACAAGCTGCAATGGAATCGCCGAAATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1213 TGGCGGTTGAATGTAATAATATCCCGGAGCAATGCAAGCATTCTCTCAAAGGCCGACTAT
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                      GATTGCTTTCAAGCTGCATTGAGATTATTGTCAAGTCTAATGTTGATATCATAACCCTTG
                                                                                                                                                                                                                      TGGATTCTGATGATGTTGAATTACTACAAATGTTGCTAAGAGAGGGGCCATACTACCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   913 TTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTGAAAGAGATCACACCAATCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGATGCATATGCTCTCCATTATGCTGTAGCGTATTGCGATGCAAAGACTACAGCAGAAC
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AGATCTCTGAATTGGTTGACAAGTTTCAGAGACACCTACTGGATATTCTTGACAAAACTG
                                                                                              CAGCAGACGATGTAATGATGGTTTTATCTGTTGCAAACATTTGTGGTAAAGCATGCGAGA
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This curve incomes the structure incomes the protection of an immunomodulated plant having a first level of resistance and involves treatment with at least 1 microbicide that confers a second level of resistance, such that the plants have a third level of resistance greater than the sum of the first two levels. The method can be applied to a wide variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect against viruses, fungi, bacteria, insects and nematodes. The method provides a high level of resistance and allows a reduction in the amount of micobicide used. Since the process involves two different methods of protection, it is unlikely that the pathogen will develop resistance to
1834 CGGCAGAAGAGCGTCAACTGAAGAAGCAAAGGTACATGGAACTTCAAGAAATTCTGACTA 1893
                AAGCATTCACTGAGGATAAAGAAGAATATGATAAGACTAACAACATCTCCTCATCTTGTT 1953
                                                                          SAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This cDNA sequence encodes the NIM-1 protein from Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                               NIM-1; noninducible immunity; systemic acquired resistance; SAR; pathogen; disease; protection; immunomodulated; plant; cereal; fruit; Vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protection of immunomodulated plants against pathogens - comprises applying microbicide to provide increase in resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
43..1824
/*tag= a
/product= NIM-1
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                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                  AAV46274 standard; cDNA; 2011
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96US-0034378.
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                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                      A. thaliana NIM-1 CDNA.
                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana.
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Score 576.8; DB 19; Length 2011; Pred. No. 7.3e-146;

26.6%; 62.7%;

Best Local Similarity

Query Match

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1056
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                            CGGAGTTTGACTACTTCGCCGACGCTAAGCTTGTGGTTTCCGGCCCGTGTAAGGAAATTC 474
                                            CGGIGCACCGGIGCATTITGTCGGCGAGGAGTCCGTTCTTTAAGAATTIGTTCTGCGGTA 534
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                                                                                                  577 IGAAAGAGCAIGAGGIGAGCIAIGAIGCIGIAAIGAGIGIAIIGGCITAITIGIAIAGIG
                                                                                                                                     AAAAGGAGAAGAATAGTAGT--------AAGGTGGAATTGAAGGAGGTGA
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     36;
     Indels
    547;
    Mismatches
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  Conservative
981;
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                                                                                                                                                                                                                                                                1703 AGGCCTTTAGTGAGGACAATTTGGAATTAGGAAATTTGTCCCTGACAGATTTGACTTCTT 1762
                                                   NIW-1; noninducible immunity; systemic acquired resistance; SAR; pathogen; disease; protection; immunomodulated; plant; cereal; fruit; vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.
                  1283 CTTTTGCAGTGGCGGCCGATGAATTGAAGATGACGCTGCTCGATCTTGAAAATAGAGTTG
         CTCTTGCTATGGCAGGCGATGATTTGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTG
                                                                             ATGGCACTTCTGAGTTCCCACTGGCTAGCATCG----GCAAAAAGATGGCTAATGCACAGA
                                                                                       GGACAACAGTAGATTTGAACGAGGCTCCTTTCAAGATAAAAGAGGAGCACTTGAATCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                     A. thaliana NIM-1 cDNA variant #1.
                                                                                                                                                                                                                                                                                                                                                   AAV46275 standard; cDNA; 2011 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "variant"
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This sequence encodes a variant NIM-1 protein from Arabidopsis thaliana. This protein is used in a method resulting in the protection of an immunomodulated plant having a first level of resistance and involves treatment with at least 1 microbicide that confers a second level of resistance, such that the plants have a third level of resistance greater than the sum of the first two levels. The method can be applied to a wide variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect against viruses, fungi, bacteria, insects and nematodes. The method approvides a high level of resistance and allows a reduction in the amount of micobicide used. Since the process involves two different methods of protection, it is unlikely that the pathogen will develop resistance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 576.8; DB 19; Length 2011;
Pred. No. 7.3e-146;
0; Mismatches 547; Indels 36;
                                                                                                                                               SJ;
                                                                                                                                                                                                                                                                                            Protection of immunomodulated plants against pathogens applying microbicide to provide increase in resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2011 BP; 563 A; 417 C; 474 G; 557 T; 0 other;
                                                                                                                                               Uknes
                                                                                                                                               Ryals JA,
                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 116-120; 164pp; English.
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                                                                                                                                                  Friedrich LB, Molina Fernandez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.6%;
illarity 62.7%;
Conservative
97US-0035024
96US-0034378
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                                                                                                                                                                                                         WPI; 1998-388119/33.
                                                                                  (NOVS ) NOVARTIS AG.
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us-08-908-884-13.rng

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ATGATGCATATGCTCTCCATTATGCTGTAGCGTATTGCGATGCAAAGACTACAGCAGAAC 1176
                                                                                                                                                                         TICTAGAICTIGCACTIGCTGAIATIAATCAICAAAATTCAAGGGGATACACGGTGCTGC 1236
                                                                                                                                                                                                                                                           1043 ATGTTGCTGCGATGCGGAAGGAGCCACAATTGATACTATCTCTATTGGAAAAAGGTGCAA 1102
                                                                                                                                                                                                                                                                                        1297 GACCTTCTGATCTGACATCCGATGGAAGAAAGCACTTCAAATCGCCAAGAGGCTCACTA 1356
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997 TACAAGGGCCTGAAAGCAACGGTTTTCCTGATAAACATGTTAAGAGGATACATAGGGCAT 1056
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                   1223 GTGTAGAAATACTAGAGCAAGAAGAAGAAGAACAAAAATTCCTAGAGATGTTCCTCCT
                                                                                                                                                                                                                                                                                                                                                1357 GGCTTGTGGATTTCAGTAAGTCTCCGGAGGAAGGAAAATCTGCTTCGAATGATCGCTTAT
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                                                         TGGATTCTGATGATGTTGATTACTACAAATGTTGCTAAGAGAGGGGGCATACTACCCTAG
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AAV43661 standard; cDNA; 2011 BP.

AAV43661 ID AAV

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inducible immunity-1 (NIM) protein. Sequences shown in AAV43661 to
AAV43665 represent variants of the NIM1 CDNA. The invention provides a
chimeric gene comprising a promoter active in plants operatively linked
to a DNA molecule that encodes an altered form of the NIM1 protein. Plant
c calls stably transformed with a recombinant vector comprising such a
chimeric gene have a broad spectrum of disease resistance. The altered
c himeric gene have a broad spectrum of disease resistance. The altered
c himeric gene have a broad spectrum of disease resistance. The altered
c himeric gene have a broad spectrum of disease resistance.
CC acquired resistance (SAR) signal transduction pathway. The transgenic
plants transformed with an altered NuM1 gene exhibits constitutive SAR
expression which is higher in the transformed plants than in a wild-type
plant. The products can be used for producing plants with a broad
c spectrum disease resistance. Overexpression of NIM1 minics the effects
c finducer. compounds that induce constitutive immunity (CIM) phenotype
c in plants. The inventions can be used with plants such as rice, wheat,
barley, rye, corn, potato, carrot, sweet potato, sugar beet, bean, pea,
chicory, lettuce, cabbage, cauliflower, broccoli, turnip, radish,
spinach, asparagus, onion, garlic, eggplant, pepper, celery, carrot,
spinach, asparagus, onion, garlic, eggplant, pepper, celery, carrot,
c squash, pumpkin, zucchini, cucumber, saple, pear, quince, melen, plum,
cherry, peach, nectarine, apricot, strawberry, grape, raspberry,
c blackberry, pineapple, avocado, papaya, mango, banana, soybean, tobacco,
                                                                                                                           Non-inducible immunity-1 gene; NIM1 gene; disease resistance; mutant; transgenic plant; SAR; systemic acquired resistance; CIM; pathogen; constitutive immunity; agriculture; variant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of non-inducible immunity-1 gene - for transforming plants to produce transgenic plants having a broad spectrum disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This cDNA encodes an altered form of the Arabidopsis thaliana non
                                                                                        Non-inducible immunity-1 (NIM1) protein variant 1 encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Steiner HY;
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/note= "wild type TCG is replaced by GCG"
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                                                                                                                                                                                                                                                                                                               "NIM1 protein variant 1"
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                                                                                                                                                                                                                                                           Location/Qualifiers
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27-DEC-1996;
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tomato, sorghum and sugarcane. The plants produced are resistant to plant pathogens such as viruses, virolds, fungi, bacteria, insects such as aphids and lepidoptera and nematodes. The plants produced can be used in agriculture.
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                                                                                                                                                                                                                                                                                                                                                                                  817 CAGCAGACGATGTAATGATGGTTTTATCTGTTGCAAACATTTGTGGTAAAGCATGCGAGA
                                                                                            36;
                                                                        Score 576.8; DB 19; Length 2011; Pred. No. 7.3e-146;
                                                                                            Indels
                                                       Sequence 2011 BP; 563 A; 417 C; 474 G; 557 T; 0 other;
                                                                                   Pred. No. 7.3e-146;
0; Mismatches 547;
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ilarity 62.7%;
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                                                                  GCCTGGCTAAACTCCTTTTTCCAATGGAAGCTAAAGTTGCAATGGACATTGCTCAAGTTG
                                                                                                                                                                                                                                                                                                                             1523 TAAAAGCGCTTTCTAAAACCGTGGAACTCGGGAAACGATTCTTCCCGGCGTTTTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1774 ITCTAAATAAGATCATGGATGCTGATGACTTGTCTGAGATAGCTTACATGGGAATGATA
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                                                                                                                                                                                                               CTCTTGCTATGGCAGGCGATGATTTGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGACAACAGTAGATTTGAACGAGGCTCCTTTCAAGATAAAAGAGGAGCACTTGAATCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1894 AAGCATTCACTGAGGATAAAGAAGAATATGATAAGACTAACAACATCTCCTCATCTTTT
                                            GGCTTGTGGATTTCAGTAAGTCTCCGGAGGAAGGAAAATCTGCTTCGAATGATCGGTTAT
                                                                                                                                                                                                                                                                                                                                                                                       ATGCCACTTCTGAGTTCCCACTGCCTAGCATCG---GCAAAAAGATGGCTAATGCACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S. tuberosum NIM1 homologue coding sequence SEQ ID NO: 45.
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Page 15

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The present invention is concerned with the isolation of NIMI homologues and their coding sequences from Arabidopsis thaliana, Brassica napus, Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus annous and Solanum tuberosum. NIMI is one of the proteins involved in the signal transduction cascade leading to systemic acquired resistance (SAR) in plants. This gives the plants an increased resistance to disease. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene and protein can be used to produce transgenic plants resistant to diseases caused by viruses, such as tobacco or cucumber mosaic virus, ringspot virus, pelargonium leaf curl virus, red clover mottle virus, tomato bushy stunt virus, fungi, including Phythophthora parasitica and Peronospora tabacina, bacteria such as Pseudomonas syringae and Ptabaci, insects, including aphids and lepidoptera and nematodes such as Meloidogyne incognita. In particular they can be used against disease
                                                                                                                                                                                                                                                                     Novel plant genes for enhancing systemic acquired resistance gene expression and broad spectrum disease resistance in plants, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 653 BP; 200 A; 124 C; 140 G; 187 T; 2 other;
                                                                                                                                                                               Mengiste T;
                                                                                                                  ) NOVARTIS AG.
) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                           Willits MG,
                                                                                                                                                                                                                                                                                                               homologues of Arabidopsis NIM1 gene
                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 115; 152pp; English.
                                      2000WO-EP01978.
                                                                           99US-0265149
                                                                                                                                                                           Weislo LJ,
                                                                                                                                                                                                             2000-594322/56.
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                                                                                                                                                                                                                                P-PSDB; AAB27316
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                                    07-MAR-2000;
                                                                         09-MAR-1999;
14-SEP-2000
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                                                                                               ATTGTAAAACAAATTACTGATTCACGAGCGGAACTTGGTCTACAAGGGCCTGAAAGCAAC 1016
                                                                                                                                             GGTTTTCCTGATAAACATGTTAAGAGGATACATAGGGCATTGGATTCTGATGATGTTGAA 1076
                                                                                                                                                                                            Tractacaaatgttgctaagaggggggtactacctagatgatgcatatgctcccat 1136
                                                                                                                                                                                                                                          TATGCTGTAGCGTATTGCGATGCAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCT 1196
                                                                                                                                                                                                                                                                                         1197 GATATTAATCATCAAAATTCAAGGGGATACACGGTGCTGCATGTTGCAGCCATGAGGAAA 1256
                                                                                                                                                                                                                                                                                                                                         1257 GAGCCTAAAATTGTAGTGTCCCTTTTAACCAAAGGAGCTAGACCTTCTGATCTGACATCC 1316
                                                                                                             897 GAGATTATTGTCAAGTCTAATGTTGATATCATAACCCTTGATAAAGCCTTGCCTCATGAC 956
                                                                                                                                                                                                          241 TATGCTGTAGCATATTGCGATGCAAAGACTACAGCAGAACTTTTAGATCTTTCACTTGCT 300
                                                                                                                                                                                                                                                                                                       Score 575.4; DB 21; Length 653;
Pred. No. 1e-145;
                          48; Indels
                          2; Mismatches
   26.5%;
92.3%;
                           Conservative
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The invention relates to rice proteins (AAB29749-B29757) and the nucleotides encoding the proteins (AAC81456-C81464), which are involved in the induction of systemic acquired resistance (SAR), a general plant resistance response that can be induced during a local infection by an avirulent pathogen. A rice cDNA library was screened using the yeast two hybrid system with Arabidopsis NRP1 cDNA as bait, and the rice proteins hym (proline rich NPR1 interactor; AAB29749) and MN1 (AAB29758) were identified as interacting with Arabidopsis NPR1. The rice cDNA library was then rescreened using rice PNI cDNA or rice MN1 CDNA as bait. Rice NH1 and NH2 (NPR homologues I and-2; AAB29753), and a protein with no protein (AAB29754) were identified as interacting with PNI convn homology (AAB29754) were identified as interacting with PNI AAB29755, AAB29755, and a protein with homology (AAB29755) and rice ARPA (a protein with homology to rat microtubule-associated protein; AAB29757) were found to interact with and rice ARPA in invention additionally encompasses irangenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plants comprising an expression cassetteen of the invention, and a method for enhancing resistance to pathogens in a plant by introducing the expression cassette into the plant, and selecting the plant with enhanced resistance. The rice SAR-associated nucleic acids and proteins are useful for enhancing plant resistance to pathogens such as viruses, bacteria, nematodes, inngi or insects. The present sequence represents cDNA encoding rice NHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rice; NH1; NPR1 homologue 1; PNI interactor; SAR; bZ1P protein;
systemic acquired resistance; yeast two-hybrid system; transgenic plant;
pathogen resistance; virus; bacterium; nematode; fungus; insect; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encodes
                                                                            GCAGAAAGAAGACCCTCTGCTAGGAGAAGCTTCTGTATCTCTTGCTATGGCAGGCGAT 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rice proline rich NPR1 interactor proteins, polypeptides interacting with PNI or MNI, and bZIP protein interacting with Arabidopsis NPR1
1377 TCTCCGGAGGAAAAATCTGCTTCGAATGATCGGTTATGCATTGAGATTCTGGAGCAA
                    GATITGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTGGCCTGGCTAAACT 1549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acid construct for enhancing pathogen resistance,
                                                                                                                                                                             Rice NPR1 homologue 1 (NH1) cDNA, SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; Page 31; 44pp; English.
                                                                                                                                                                                                                                                                                          AAC81457 standard; cDNA; 2040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ronald P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-090867/10.
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The present sequence is a putative version of the rice negatively phytochrome regulated 1 (NPR1) gene coding sequence. It was isolated by screening a leaf cDNA library for those sequences which were similar to the NPR1 gene from Arabidopsis thaliana. The protein is involved in systemic acquired resistance and this gene can be used to create transgenic plants which are protected from pathogens. It can also
                                                                                                                                                                                                                                                                  CACTCTCTAGGAACTGTAGAACTTGGAAAACGCTTCTTTCCACGTTGTTCAGAAGTTCTAA 1779
                                                                                                                                                   1496 CACTCTCCAAAACAGTGGAGCTCGGGAAACGCTTTTTCCCGCGATGTTCGAACGTGCTCG 1555
                                                                                                                                                                                                           1840 AAGAGCGTCAACTGAAGAAGCAAAGGTACATGGAACTTCAAGAAATTCTGACTAAAGCAT 1899
1316 TGGCAAGGATTATGTTTCCGATGGAGGCAAGAGTAGCAATGGATATTGCTCAAGTGGATG 1375
                                                   GAACTITGGAATTTAACCTGGGTTCTGGTGCAAATCCACCTCCTGAAAGACAACGGACAA 1435
                                                                                                                                                                                          ATAAGATCATGGATGCTGATGACTTGTCTGAGATAGCTTACATGGGGAATGATACGGCAG 1839
                           GCACTTCTGAGTTCCCACTGGCTAGCATCGGCAAAAAGATGGCTAATGCACAGAGGACAA
                                                                                CAGTAGATTTGAACGAGGCTCCTTTCAAGATAAAAGAGGAGCACTTGAATCGGCTTAGAG
                                                                                             1436 CTGTTGATCTAAATGAAAGTCCTTTCATAATGAAAGAAGAACACTTAGCTCGGATGACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rice putative negatively phytochrome regulated 1 (NPR1) gene
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                                             2040;
                                                                      15;
                                           Score 563.4; DB 22; Length Pred. No. 3.2e-142; 0; Mismatches 476; Indels
                  BP; 501 A; 525 C; 553 G; 461 T; 0 other;
                                            25.9%;
64.3%;
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                  Sequence 2040
                                                                       Matches 884;
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                                                                                     15;
                                                             DB 21; Length 2194;
                                                          Score 558.6; DB 21; Length
Pred. No. 6.6e-141;
0; Mismatches 479; Indels
                                 Sequence 2194 BP; 510 A; 586 C; 617 G; 481 T; 0 other;
                                                         25.7%;
64.1%;
                                                                       Best Local Similarity 64.1
Matches 881; Conservative
                                                            Query Match
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                                                    CACTCTCTAGAACTGTAGAACTTGGAAAAGGCTTCTTTCCACGTTGTTCAGAAGTTCTAA
                                                                                                                                      GCACTTCTGAGTTCCCACTGGCTAGCATCGGCAAAAAGATGGCTAATGCACAGAGGACAA
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/note= "variant"
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This sequence encodes a truncated variant NIM-1 protein from Arabidopsis thaliana. This protein is used in a method resulting in the protection of an immunomodulated plant having a first level of resistance and involves treatment with at least 1 microbicide that confers a second level of resistance, such that the plants have a third level of resistance greater than the sum of the first two levels. The method can be applied to a wide variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect against viruses, fungi, bacteria, insects and nematodes. The method of micobicide used. Since the process involves two different methods of protection, it is unlikely that the pathogen will develop resistance to 25255555555555x8

Sequence 1597 BP; 467 A; 304 C; 381 G; 445 T; 0 other;

GTAAAACAAATTACTGATTCACGAGCGGAACTTGGTCTACAAGGGCCTGAAAGCAACGGT 1019 1020 TITCCTGATAAACATGTTAAGAGGATACATAGGGCATTGGATTCTGATGATGTTGAATTA 1079 1080 CTACAAAIGTIGCTAAGAGGGGCATACTACCTAGATGATGCATATGCTCCCATTAT 1139 GCTGTAGCGTATTGCGATGCAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCTGAT 1199 200 ATTAATCATCAAAATTCAAGGGGATACACGGTGCTGCATGTTGCAGCCATGAGGAAAGAG 1259 CCTAAAATTGTAGTGTCCCTTTTAACCAAAGGAGCTAGACCTTCTGATCTGACATCCGAT 1319 GGAAGAAAAGCACTICAAAICGCCAAGAGGCTCACIAGGCITGIGGAITITCAGIAAGICT 1379 GGTAGAACCGCACTCATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATATC 771 GTCAAGTTGCTTTTGAAAGAGGATCACAACCAATCTAGATGATGCGTGTGCTCTTCATTTC 531 GATGTGTGTGTTTGTGTGGACAATGACTGCTCTCATGTGGCCTTGTAGGCCAGCTGTGGCA 719 184 TATCAGAGGCACTTATTGGACGTTGTAGACAAGTTGTTATAGAGGACACATTGGTTATA 243 4 GATTCGGTTGTGACTGTTTTGGCTTATGTTTACAGCAGCAGCAGTGAGACCGCCGCCTAAA TTATCTGTTGCAAACATTTGTGGTAAAGCATGCGAGAGATTGCTTTCAAGCTGCATTGAG 244 CTCAAGCTTGCTAATATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGATGTAAAGAG CCACAATTGATACTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAA 600 GATGCTGTAATGAGTGTATTGGCTTATTTGTATAGTGGTAAAGTTAGGCCTTCACCTAAA TTCCTGGTTGAGGTTTTGTACACATCATTTACCTTTCAGATCTCTGAATTGGTTGACAAG TITCAGAGACACCTACTGGATATICTTGACAAAACTGCAGCAGACGATGTAATGATGGTT ATTATTGTCAAGTCTAATGTTGATATCATAACCCTTGATAAAGCCTTGCCTCATGACATT DB 19; Length 1597; Indels 0; Mismatches 476; Score 549.4; DB 1 Pred. No. 1.8e-138 25.3%; 63.9%; Matches 870; Conservative Local Similarity 099 124 780 900 304 096 419 64 720 g g g 8 ö g à g ò q ö g ò g ò g Qγ Q ò å ŏ ò ò ò g

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1857 AAGCAAAGGTACATGGAACTTCAAGAAATTCTGACTAAAGCATTCACTGAGGATAAAGAA 1916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resistance; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Non-inducible immunity-1 gene; NIM1 gene; disease resistance; mutan transgenic plant; SAR; systemic acquired resistance; CIM; pathogen; constitutive immunity; agriculture; variant; ss.
                                                                                                                                                                 1072 GCACCTITCAGAATCCTAGAAGAGCATCAAAGTAGACTAAAAGCGTTTCTAAAAACCGTG
                                                                                                                                                                                                                                                                                                                                                   1132 GAACTCGGGAAACGATTCTTCCGGGGCTTTTGGCAGTGCTCGACCAGATTATGAACTGT
772 CCGGAGCAATGCAAGCATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAA
                             1440 GAAAGAAGAGCCCTCTGCTAGGAGAAGCTTCTGTATCTCTTGCTATGGCAGGCGATGAT
                                           1560 ATGGAAGCTAAAGTTGCAATGGACATTGCTCAAGTTGATGGCACTTCTGAGTTCCCACTG
                                                                                                                                                                                                           1620 GCTAGCATCG---GCAAAAAGATGGCTAATGCACAGAGGACAACAGTAGATTTGAACGAG
                                                                                                                                                                                                                                                                    1677 GCTCCTTTCAAGATAAAAGAGGAGCACTTGAATCGGCTTAGAGCACTCTAGAACTGTA
                                                                                                                                                                                                                                                                                                                                                                                       GATGACTTGTCTGAGATAGCTTACATGGGAATGATACGGCAGAAGAGCGTCAACTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                   1192 GAGGACTTGACTCAACTGGCTTGCGGAGAAGACGACACTGCTGAAAACGACTACAAAAG
                                                                                      TTGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTGGCCTGGCTAAACTCCTTTTTCCA
                                                                                                                                                                                                                                                                                                                             GAACTTGGAAAACGCTTCTTTCCACGTTGTTCAGAAGTTCTAAATAAGATCATGGATGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Non-inducible immunity-1 (NIM1) protein variant 2 encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a /product= "NIM1 protein variant 2" /product= "N-terminal deletion compared /note= "NIM1 sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1312 GAATTAGGAAATTTGTCCCTGACAGATTCGACTTCTTCCAC 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1917 GAATATGATAAGACTAACAACATCTCCTCATCTTGTTCCTC 1957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV43662 standard; cDNA; 1597
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96US-0033177.
96US-0034379.
96US-0034382.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-DEC-1996;
27-DEC-1996;
27-DEC-1996;
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condicible immunity-1 (NIM) protein. Sequences shown in AAV33661 to AAV4365 represent variants of the NIM1 CDNA. The invention provides a chiefful immunity-1 (NIM1) protein. Sequences shown in AAV43661 to AAV4365 represent variants of the NIM1 CDNA. The invention provides a chiefful stably transformed with a recombinant vector comprising such a chiefful stably transformed with a recombinant vector comprising such a chiefful stably transformed with a recombinant vector comprising such a chimeric gene have a broad spectrum of disease resistance. The altered compined resistance (SAR) signal transduction pathway. The transgenic plants transformed with an altered NIM1 gene exhibits constitutive SAR expression which is higher in the transformed plants than in a wild-type plant. The products can be used for producing plants with a broad spectrum disease resistance. Overexpression of NIM1 mimics the effects of inducer compounds that induce constitutive immunity (CIM) phenotype in plants. The inventions can be used with plants such as rice, wheat, barley, rye, corn, potato, carrot, sweet potato, sugar beet, bean, pea, chicory, lettuce, cabbage, cauliflower, broccoll, turnip, radish, spanagus, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, quince, melon, plum, chemical application, apricot, strawberry, grape, raspbarry, comato, sorghum and sugarcene. The plants produced are resistant to a plackberry, planeapple, avocado, papaga, mango, banana, soybean, tobacco, comato, sorghum and sugarcene. The plants produced are resistant to a paridoch, as white such as virtuely.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plant pathogens such as viruses, viroids, fungi, bacteria, insects such as aphids and lepidoptera and nematodes. The plants produced can be used
                                                                                                                                                                                                                                                                                                               Use of non-inducible immunity-1 gene - for transforming plants to produce transgenic plants having a broad spectrum disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                               This cDNA encodes an altered form of the Arabidopsis thaliana Inducible immunity-1 (NIM1) protein. Sequences shown in AAV436
                                                                                                                                                              Steiner HY;
                                                                                                                                                              Ryals JA,
                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Pages 149-152; 205pp; English.
                                                                                                                                                        Lawton KA,
97US-0034730.
97US-0035021.
97US-0035022.
                                                                                                                                                           Hunt MD,
                                                                                                                                                                                                                                     WPI; 1998-348536/30.
                                                                                                     (NOVS ) NOVARTIS AG
                                                                                                                                                                                                                                                              P-PSDB; AAW61984
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                                                                                                                                                      Friedrich LB,
                                                   10-JAN-1997;
                           10-JAN-1997
                                                                                                                                                                                 SJ;
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Sequence 1597 BP; 467 A; 304 C; 381 G; 445 T; 0 other; Query Match

2 243 303 GATGCTGTAATGAGTGTATTGGCTTATTTGTATAGTGGTAAAGTTAGGCCTTCACCTAAA 659 GAIGIGIGITIGIGIGACAAIGACIGCICICAIGIGGCCIIGIAGGCCAGCIGIGGCA 719 TICCTGGTTGAGGTTTTGTACACATCATTTACCTTTCAGATCTCTGAATTGGTTGACAAG 779 Gaps 63 TATCAGAGGCACTTATTGGACGTTGTAGAGTTGTTATAGAGGACACATTGGTATATA TTATCTGTTGCAAACATTTGTGGTAAAGCATGCGAGAGATTGCTTTCAAGCTGCATTGAG TITCAGAGACACCTACTGGATATICTTGACAAAACTGCAGCAGACGATGTAATGATGGTT 124 ITCAIGITGGAGGITCICIAITIGGCITICAICITCAAGAICCCIGAAITAAITACICIC ATTATTGTCAAGTCTAATGTTGATATCATAACCCTTGATAAAGCCTTGCTCATGACATT CTCAAGCTIGCTAATATATGTGGTAAAGCTIGTATGAAGCTATTGGATAGATGTAAAGAG Score 549.4; DB 19; Length 1597; Pred. No. 1.8e-138; 15; 0; Mismatches 476; Indels 25.3%; Best Local Similarity 63.9 Matches 870; Conservative 009 4 099 64 720 780 184 900 ŏ g δ g δy 셤 qq ŏ qq ò οy

Search completed: October 7, 2002, 22:58:47

Job time : 253.181 secs

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304

1079 1199 1619 GTAAAAACAAATTACTGATTCACGAGCGGAACTTGGTCTACAAGGGCCTGAAAGCAACGGT 1019 1080 CTACAAATGTTGCTAAGAGAGGGGCATACTACCTAGATGATGCATATGCTCTCCATTAT 1139 1200 ATTAATCATCAAAATTCAAGGGGATACACGGTGCTGCATGTTGCAGCCATGAGGAAAGAG 1259 GGAAGAAAAGCACTTCAAATCGCCAAGAGGCTCACTAGGCTTGTGGATTTCAGTAAGTCT 1379 GAAAGAAGAAGCCTCTGCTAGGAGAAGCTTCTGTATCTTTGCTATGGCAGGCGATGAT 1499 1620 GCTAGCATCG---GCAAAAAGATGGCTAATGCACAGAGGACAACAGTAGATTTGAACGAG 1676 GAACTIGGAAAACGCTTCTTTCCACGTTGTTCAGAAGTTCTAAATAAGATCATGGATGCT 1796 GATGACTTGTCTGAGATAGCTTACATGGGGAATGATACGGCAGAAGAGCGTCAACTGAAG 1856 AAGCAAAGGTACATGGAACTTCAAGAAATTCTGACTAAAGCATTCACTGAGGATAAAGAA 1916 1192 GAGGACTTGACTCAACTGGCTTGCGGAGAAGACGACACTGCTGAGAAACGACTACAAAAG 1251 AAGCAAAGGTACATGGAAATACAAGAGACACTAAAGAAGGCCTTTAGTGAGGACAATTTG 1311 471 651 951 -----AGAAACATGTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTA 1140 GCTGTAGCGTATTGCGATGCAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCTGAT GCTCCTTTCAAGATAAAAGAGGAGCACTTGAATCGGCTTAGAGCACTCTAGAACTGTA 1020 TTTCCTGATAAACATGTTAAGAGGATACATAGGGCATTGGATTCTGATGTTGAATTA 1260 CCTAAAATTGTAGTGTCCCTTTTAACCAAAGGAGCTAGACCTTCTGATCTGACATCCGAT GGTAGAACCGCACTCATGATCGCAAAACAAGCCACTATGGCGGTTGAATGATAATATC GACAAACGAGAACAAATTCCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAA TIGCGIATGAAGCIGTIATACCTTGAAAATAGAGTIGGCCTGGCTAAACTCCTTTTTTCCA ATGGAAGCTAAAAGTTGCAATGGACATTGCTCAAGTTGATGGCACTTCTGAGTTCCCACTG 1917 GAATATGATAAGACTAACAACATCTCCTCATCTTGTTCCTC 1957 712 832 096 1320 1380 1440 1500 1560 952 1677 1072 1737 1797 1857 1252 g qq ò Db QY g ŏ δŏ qq QY 염 δ g δy g δ d δ ΩD à g ολ δ Dp q qq q ò ò

us-08-908-884-13.rni

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PRIOR ADPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
ATTORNEY/ACENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
                                                                                                                                                                                                     October 7, 2002, 22:39:34; Search time 47.2395 Seconds (without alignments) 11293.859 Million cell updates/sec
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Sequence 220,
Sequence 2, Apl
Sequence 3, Apl
                                                                                                                                                                                                                                                                                                                                                     sequence 6, A sequence 7, A sequence 9, A sequence 11, Sequence 11, Sequence 13, Sequence 1, A sequence 1, A sequence 1, A sequence 15, Sequence 15, Sequence 16, Sequence 16,
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Sequence 7,
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Patent No.
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2: /cgn2_6/ptodata/2/lna/5B_COMB.seg:*
3: /cgn2_6/ptodata/2/lna/6A_COMB.seg:*
4: /cgn2_6/ptodata/2/lna/6B_COMB.seg:*
5: /cgn2_6/ptodata/2/lna/PCTUS_COMB.seg:*
6: /cgn2_6/ptodata/2/lna/PcTUS_COMB.seg:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-630-915A-220
US-08-506-340A-2
US-09-078-294-3
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US-08-996-685-9
US-08-989-478-19
US-08-989-478-11
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US-08-989-478-11
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US-08-996-685-15
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US-08-996-973-462-1
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Listing first 45 summaries
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Sequence 389, Ap Sequence 389, Ap Sequence 388, Ap Sequence 7, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 13, Appl Sequence 14, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 18, Appl Sequence 18, Appl		CONFERRING
08-998-416-595 09-328-111-388 08-922-061-4 08-625-061-4 08-621-997-3 08-621-997-3 08-621-493-3 08-965-688-3 08-965-688-3 08-934-959-7 08-492-459-13 08-492-459-13 08-492-459-13 08-411-27 09-368-431-27 09-368-431-27 09-368-935-2	ALIGNMENTS	RMS OF THE NIM1 GENE SISTANCE IN PLANTS Corporation a a 9,478 4,379 4,379 4,382
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COPHER INFORMATION: /product= "NIM1 protein"
US-08-989-478-6
                                                                                                                                                                     "NIM1 CDNA
                                                                                       TOPOLOGY: linear
ONGECULE TYPE: CDNA
ONIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
TELECOMMUNICATION INFORMATION:
TELEFAN: (919) 541-8587
TELEFAN: (919) 541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2011 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 1..2011
OTHER INFORMATION: /note=
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62.7%;
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ATGTTGCAGCCATGAGGAAAGAGCCTAAAATTGTAGTGTCCCTTTTAACCAAAGGAGCTA
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Patent No. 5986082
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Uknes, Scott
APPLICANT: Hunt, Michelle
APPLICANT: Steiner, Henry-York
APPLICANT: Ryals, John
TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "altered form of NIM1" /note= "Serine residues at amino acid positions 55 and 59 wild-type NIM1 gene product have been changed to Alanine residues".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415 CGGAGTTTGACTACTTCGCCGACGCTAAGCTTGTGGTTTCCGGCCCGTGTAAGGAAATTC 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.6%; Score 576.8; DB 2; Length 2011; 62.7%; Pred. No. 1.5e-155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.30
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                                No. 5986082artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/034,730 FILING DATE: 10-JAN-1997
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                     CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/989,478
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/033,177 FILING DATE: 13-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UMBER: US 60/035,021
10-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/035,022
                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                           f: 3054 Cornwallis Road
Research Triangle Park
: No. 5986082th Carolina
XY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 7:
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LOCATION: 205..217
OTHER INFORMATION: /not
OTHER INFORMATION: char
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                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
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                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 43..1824
OTHER INFORMATION:
OTHER INFORMATION:
OF SEQUENCES:
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OTHER INFORMATION:
FEATURE:
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                                  ADDRESSEE:
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981;
                                                                                                  COUNTRY:
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Matches
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                                                                                                                          1597 ATGGCACTTCTGAGTTCCCACTGGCTAGCATCG---GCAAAAAGATGGCTAATGCACAGA
                                                                                 TTCTAAATAAGATCATGGATGCTGATGACTTGTCTGAGATAGCTTACATGGGGAATGATA
                             1403 AGGGAACATGTGAGTTCATAGTGACTAGCCTCGAGCCTGACCGTCTCACTGGTACGAAGA
                                                                                                                                                                                                                                                       CGGCAGAAGAGCGTCAACTGAAGAAGCAAAGGTACATGGAACTTCAAGAAATTCTGACTA
                                                               GGACAACAGTAGATTTGAACGAGGCTCCTTTCAAGATAAAAGAGGAGCACTTGAATCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kessmann, Helmut
APPLICANT: Oostendorp, Michael
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: No. 6031153artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6031153th Carolina
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APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
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APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,378
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Friedrich, Leslie
Uknes, Scott
Molina, Antonio
Ruess, Wilhelm
Knauf-Beiter, Gertrude
Kung, Ruth
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BELIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6031153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ryals, John
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                                                                                                                                                                                                                                                                                                                                                                                CCTC 1957
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    475 CGGTGCACCGGTGCATTTTGTCGCGAGGAGTCCGTTCTTTAAGAATTTGTTCTGCGGTA 534
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                                                                                                                                                                                                                                                                                                                                                              NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PE/5-21215/P1/CGC1912
TELECOMOUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "NIM1 cDNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 576.8; DB 3;
Pred. No. 1.5e-155;
0; Mismatches 547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "NIM1 protein'
               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-UAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
                                                                                                                                                                                      FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,024
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/875,015
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ilarity 62.7%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (919) 541-8587
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ATTORNEY/AGENT INFORMATION:
FILING DATE: 27-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2011 base pairs
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LOCATION: 1..2011
OTHER INFORMATION: /not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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EDNESS: single
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; OTHER INFORMATION:
US-08-996-685-6
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ORIGINAL SOURCE:
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Matches 981;
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                                                                                                                                                                                                                                                                               ATGATGCATATGCTCTCCATTATGCTGTAGCGTATTGCGATGCAAAGACTACAGCAGAAC 1176
                                                                                                                                                                                                                                                                                                                                    TTCTAGATCTTGCACTTGCTGATATTAATCATCAAAATTCAAGGGGATACACGGTGCTGC 1236
                                                                                                                                                                                                                                                                                                                                                                                        ATGTTGCAGCCATGAGGAAAGAGCCTAAAATTGTAGTGTCCCTTTTAACCAAAGGAGCTA 1296
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                                                                                                                                            AAAAGTCATTGCCGGAAGAGCTTGTTAAAGAGATAATTGATAGACGTAAAAGACTTGGTT 814
        817 CAGCAGACGATGTAATGATGGTTTTATCTGTTGCAAACATTTGTGGTAAAGCATGCGAGA
                                                              GATTGCTTTCAAGCTGCATTGAGATTATTGTCAAGTCTAATGTTGATATCATAACCCTTG
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1894 AAGCATTCACTGAGGATAAAGAAGAATATGATAAGACTAACAACATCTCCTCATCTTGTT 1953
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TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEE: No. 6031153artis Corporation
: 3054 Cornwallis Road
Research Triangle Park
No. 6031153th Carolina
Y: USA
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PRIOR APPLICATION DATA:
APPLICATION APPLICATION DATA:
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FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/034,730
                                                                                                                                                                                                                                                      Ryals, John
Friedrich, Leslie
Uknes, Scott
Molina, Antonio
Ruess, Wilhelm
Knauf-Balter, Gertrude
Kung, Ruth
Kessmann, Helmut
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10-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/996,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
                                                                                                                                                                                                  Sequence 7, Application US/08996685 Patent No. 6031153 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
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FILING DATE: 10-JAN
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APPLICANT:
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STATE:
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                                              ATGATGCATATGCTCTCCATTATGCTGTAGCGTATTGCGATGCAAAGACTACAGCAGAAC
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US-08-989-478-9
; Sequence 9, Application US/08989478
; Patent No. 5986082
; GENERAL INFORMATION:
; APPLICANT: Uknes, Scott
; APPLICANT: Hunt, Michalle
; APPLICANT: Steiner, Henry-York
; APPLICANT: Steiner, Henry-York
; APPLICANT: Ryals, John
; ITILE OF INVENTION: ALTERED FORMS
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/note- "Serine residues at amino acid positions 55 and 59
wild-type NIM1 gene product have been changed to Alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to wild-type sequence."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 CGCCGGATGATTTCTACAGCGACGCTAAGCTTGTTCTCTCCGAC---GGCCGGGAAGTTT 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGATCTCTGAATTGGTTGACAAGTTTCAGAGACACCTACTGGATATTCTTGACAAAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2011;
                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 43..182
LOCATION: 43..182
COTHER INFORMATION: /note= "Serine residues at amino acid OTHER INFORMATION: wild-type NIMI gene product have been OTHER INFORMATION: residues."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 205..217
OTHER INFORMATION: Changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER INFORMATION: changed from T's to G's compared to NOTHER IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.6%; Score 576.8; DB 3;
Llarity 62.7%; Pred. No. 1.5e-155;
Conservative 0; Mismatches 547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (919) 541-8689
INFORMATION FOR SEC ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2011 base pairs
TYPE: nucleic acid
STRANDEDMESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
    (919) 541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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hes 981;
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Matches
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/product= "Altered form of NIM1" /note= "N-terminal deletion compared to wild-type NIM1 sequence."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITCCTGGTTGAGGTTTTGTACACATCATTTACCTTTCAGATCTCTGAATTGGTTGACAAG 779
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                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,478
DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF/5-21214/P1/CGC1911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atch 25.3%; Score 549.4; DB 2; cal Similarity 63.9%; Pred. No. 9.6e-148; 870; Conservative 0; Mismatches 476;
                                                   Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/034,730 FILING DATE: 10-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                US 60/034,379
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US 60/035,022
                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                             SEE: No. 5986082artis C
: 3054 Cornwallis Road
Research Triangle Park
No. 5986082th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Meigs, J. Timothy
TimpER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PFT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEPAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                 FILING APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 60
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60
FILING DATE: 27-DEC-1996
:IOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
            OF SEQUENCES:
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OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 1..1
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                                                                                                                    USA
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                                                                                                                                 27709
                                               ADDRESSEE:
STREET: 30
                                                                                                                  COUNTRY:
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960 GTAAAACAAATTACTGATTCACGAGCGGAACTTGGTCTACAAGGGCCTGAAAGCAACGGT 1019 1439 1080 CTACAAATGTTGCTAAGAGGGGGATACTACCCTAGATGATGCATATGCTCTCCATTAT 1139 1140 GCTGTAGCGTATTGCGATGCAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCTGAT 1199 1260 CCTAAAATTGTAGTGTCCCTTTTAACCAAAGGAGCTAGACCTTCTGATCTGACATCCGAT 1319 1379 1440 GAAAGAAGACCCTCTGCTAGGAGAAGCTTCTGTATCTCTTTGCTATGGCAGGCGATGAT 1499 1560 AIGGAAGCIAAAGTIGCAAIGGACAIIGCICAAGIIGAIGGCACTICIGAGIICCCACIG 1619 ACGGAAGCACAAGCTGCAATGGAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTG 1011 TTGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTGGCCTGGCTAAACTCCTTTTTCCA 1559 GCTAGCATCG---GCAAAAAGATGGCTAATGCACAGAGGACAACAGTAGATTTGAACGAG 1676 1012 ACTAGCCTCGAGCCTGACCGTCTCACTGGTACGAAGAACATCACCGGGTGTAAAGATA 1071 GAACTIGGAAAACGCTTCTTTCCACGTIGTTCAGAAGTTCTAAATAAGATCATGGATGCT 1796 GATGACTTGTCTGAGATAGCTTACATGGGGAATGATACGGCAGAAGAGCGTCAACTGAAG 1856 303 959 363 591 651 771 891 951 TITCAGAGACACCTACTGGATATTCTTGACAAAACTGCAGCAGACGATGTAATGATGGTT TTATCTGTTGCAAACATTTGTGGTAAAGCATGCGAGAGATTGCTTTCAAGCTGCATTGAG 244 CTCAAGCTTGCTAATATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGATGTAAAGAG ATTATTGTCAAGTCTAATGTTGATATCATAACCCTTGATAAAGCCTTGCCTCATGACATT 304 ATTATIGICAAGICTAATGIAGATATGGITAGICTIGAAAAGICATIGCCGGAAGAGCIT 1200 ATTAATCATCAAAATTCAAGGGGATACACGGTGCTGCATGTTGCAGCCATGAGGAAAGAG 1320 GGAAGAAAAGCACTTCAAATCGCCAAGAGGCTCACTAGGCTTGTGGATTTCAGTAAGTCT 1020 ITTCCTGATAAACATGTTAAGAGGATACATAGGGCATTGGATTCTGATGATGTATA 652 CCACAATTGATACTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAA 832 GACAAACGAGAACAAATTCCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGGCCGATGAA GCTCCTTTCAAGATAAAAGAGGAGCACTTGAATCGGCTTAGAGCACTCTCTAGAACTGTA 780 840 006 1500 952 1620 1677 1072 1737 1132 1797 1192 a δ qq ò g δ g ð g δ g δ 엄 ò d δy g g òγ g ŏ Q ŏ P ò g qq g ŏ ŏ ò δ g δλ g

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1857 AAGCAAAGGTACATGGAACTTCAAGAAATTCTGACTAAAGCATTCACTGAGGATAAAGAA 1916
               1252 AAGCAAAGGTACATGGAAATACAAGAGACACTAAAGAGGCCTTTAGTGAGACAATTG 1311
                                                                                  1917 GAATATGATAAGACTAACAACATCTCCTCATCTTGTTCCTC 1957
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OOSTENDOPP, Michael
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: No. 6031153artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6031153th Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
FRICH APPLICATION DATA:
APPLICATION NUMBER: US 60/034,378
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,024
FILING DATE: 10-0AN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/875,015
FILING DATE: 16-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/996,685 FILING DATE:
                                                                                                                                                                                                                                 Ryals, John
Friedrich, Leslie
Uknes, Scott
Molina, Antonio
Ruess, Wilhelm
Knauf-Beiter, Gertrude
Kung, Ruth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
                                                                                                                                                                                  Sequence 9, Application US/08996685
Patent No. 6031153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                        Kessmann, Helmut
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                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Ryals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NO. COUNTRY: US. ZIP: 27709
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APPLICANT:
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/product= "Altered form of NIM1" /note= "N-terminal deletion compared to wild-type NIM1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTAATCATCAAAATTCAAGGGGATACACGGTGCTGCATGTTGCAGCCATGAGGAAAGAG 1259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 CTCAAGCTTGCTAATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGATGAAAGAG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTATTGTCAAGTCTAATGTTGATATCATAACCCTTGATAAAGCCTTGCCTCATGACATT 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   532 GCTGTTGCATATTGCAATGTGAAGACCGCAACAGATCTTTAAAAACTTGATCTTGCCGAT 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           660 GATGTGTGTTTGTGTGGACAATGACTGCTCTATGTGGGCTTGTAGGCCAGCTGTGGCA 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         720 TICCIGGIIGAGGIITIGIACACAICAITIACCITICAGAICICIGAAIIGGIIGACAAG 779
                                                                                                                                                                                                                                                                                                                                                                                                                             600 GATGCTGTAATGAGTGTATTGGCTTATTTGTATAGTGGTAAAGTTAGGCCTTCACCTAAA 659
                                                                                                                                                                                                                                                                                                                                                                                       15; Gaps
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Pred. No. 9.6e-148;
0; Mismatches 476;
                                                                                                                                                                                                                                                                                        sednence.
TELEPHONE: (919) 541-8587
TELERAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1597 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                 25.3%;
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: US-08-996-685-9
                                                                                                                                                                                                                             LOCATION: 1.1410
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                            CDS
                                                                                                                                                                                                          NAME/KEY:
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Matches 870;
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1440 GAAAGAAGACCCTCTGCTAGGAAGCTTCTGTATCTCTTGCTATGGCAGGGGATGAT 1499
                                                                                                                                                                      1560 ATGGAAGCTAAAAGTTGCAATGGACATTGCTCAAGTTGATGGCACTTCTGAGTTCCCACTG 1619
                                                                                                                                                                                         1620 GCTAGCATCG----GCAAAAGATGGCTAATGCACAGAGGACAACAGTAGATTTGAACGAG 1676
                                                                                                                                                                                                                                               GATGACTTGTCTGAGATAGCTTACATGGGGAATGATACGGCAGAAGAGGGCGTCAACTGAAG 1856
                                                                                                                                                                                                                                                                                                                                                                                                                                       1251
                                                                                                                                                                                                                                                                                                       1677 GCTCCTTTCAAGATAAAAGAGGAGCACTTGAATCGGCTTAGAGCACTCTAGAACTGTA
                                                                                                                                                                                                                                                                                                                                                              1192 GAGGACTTGACTCAACTGGCTTGCGGAGAAGACGACACTGCTGAGAAACGACTACAAAAG
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                                                                                                                 TTGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTGGCCTGGCTAAACTCCTTTTTCCA
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APPLICANT: Hunt, Michelle
APPLICANT: Hunt, Michelle
APPLICANT: Steiner, Henry-York
APPLICANT: Ryals, John
TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1917 GAATATGATAAGACTAACAACATCTCCTCATCTTGTTCCTC 1957
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SOFTWARE: PATENTIA RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSE: No. 5986082artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 5986082th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/08989478 Patent No. 5986082 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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ADDRESSEE: No. 59860
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CLASSIFICATION:
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/product= "Altered form of NIM1" /note= "C-terminal deletion compared to wild-type NIM1."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    577 IGAAAGAGCAIGAGGIGAGCIAIGAIGCIGIAAIGAGIGIAIIGGCIIAIIIGIAIAGIG 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 CTAAGAAGGAGAAAAGACTCCAACAACACGCCGCCGTGAAGCTCGAGCTTAAGGAGATTG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCTIGTAGGCCAGCTGTGGCATTCCTGGTTGAGGTTTTGTACACATCATTACCTTTC 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGCAGACGATGTAATGATGGTTTTATCTGTTGCAAACATTTGTGGTAAAGCATGCGAGA 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGTGCACCGGTGCATTTTGTCGGCGAGGAGTCCGTTCTTTAAGAATTTGTTCTGCGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGATCTCTGAATTGGTTGACAAGTTTCAGAGACACCTACTGGATATTCTTGACAAAACTG
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                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 23.8%; Score 517.4; DB 2; Best Local Similarity 63.0%; Pred. No. 1.5e-138; Matches 882; Conservative 0; Mismatches 481;
                                                                      FILING DATE: 27-DEC-1996
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
FRICK APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
FRICK APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
FRICK APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
FRILK DATE: 10-JAN-1997
FRILK DATE: 10-JAN-1997
FRILK DATE: 10-JAN-1997
  US 60/034,379
                                                                                                                                                                                                                                                                                                                          NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
                         27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1608 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  535 AAAAGGAGAAGAATAGTAGT--
                  FILING DATE: 27-DEC-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
APPLICATION NUMBER:
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OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION:
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LOCATION: 43.1608
CTHER INFORMATION: /product= "Altered form of NIM1"
CTHER INFORMATION: /note= "C-terminal deletion compared to wild-type NIM1."
US-08-996-685-11
                                                                         PROTECTING PLANTS
                                                                                                                                                                                                                                                                                                                                  Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF/5-21215/P1/CGC1912
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Pred. No. 1.5e-138;
0; Mismatches 481;
                                                                                                            AUDRESSEE: No. 6031153artis Corporation STREET: 3054 COINWallis Road CITY: Research Triangle Park STATE: No. 603115344
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
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APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UMBER: 'US 60/034,378
27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JMBER: US 60/034,379
27-DEC-1996
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APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA: US 60/035,024
APPLICATION NUMBER: US 60/035,024
                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/996,685
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Knauf-Beiter, Gertrude
Kung, Ruth
Kessmann, Helmut
                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                  APPLICANT: Kung, Ruth
APPLICANT: Kessmann, Helmut
APPLICANT: Costendorp, Michael
TITLE OF INVENTION: METHOD FOR PR
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                               No. 6031153th Carolina: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 11:
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63.0%;
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APPLICATION NUMBER: US 08
FILING DATE: 16-JUL-1997
ATTORIEY/AGENT INFORMATION:
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APPLICATION NUMBER: '(FILING DATE: 27-DEC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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Matches 882; Conser
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                                                                                                                                                                                                                                      27709
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                                                                                                                      TACAAGGGCCTGAAAGCAACGGTTTTCCTGATAAACATGTTAAGAGGATACATAGGGCAT 1056
                                                                                                                                                                                                                                                                               ATGATGCATATGCTCTCCATTATGCTGTAGCGTATTGCGATGCAAAGACTACAGCAGAAC 1176
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                                                                                                                                            695 AGCTATTGGATAGATGTAAAGAGATTATTGTCAAGTCTAATGTAGATATGGTTAGTTTG 754
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Patent No. 603153
GENERAL INFORMATION:
APPLICANT: Ryals, John
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Friedrich, Leslie
Uknes, Scott
Molina, Antonio
Ruess, Wilhelm
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CGGAGTITIGACTACTICGCCGACGCTAAGCTIGIGGTTTCCGGCCCGTGTAAGGAAATTC 474
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          577 TGAAAGAGCATGAGGTGAGCTATGATGCTGTAATGAGTGTATTGGCTTATTTGTATAGTG
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                                         CGGTGCACCGGTGCATTTTGTCGCCGAGGAGTCCGTTCTTTAAGAATTTGTTGTGCGGTA
                                                                                   ----AAGGTGGAATTGAAGGAGGTGA
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CTCTTGCTATGGCAGGCGATGATTTGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTG 1536
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APPLICANT: Steinber, Henry-York
APPLICANT: Ryals, John
TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GEN
TITLE OF INVENTION: DISFASE RESISTANCE IN PLANTS
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,478
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
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10-JAN-1997
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PRIOR APPLICATION DATA: 600/CAPPELLATION NUMBER: 05 60/CAPPELL OF THE PRIOR APPLICATION NUMBER
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FILING DATE: 10-JAN
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GENERAL INFORMATION:
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                                    GAAAGAAGACCCTCTGCTAGGAGAAGCTTCTGTATCTTTGCTATGGCAGGCGATGAT 1499
                                                                                                                                                                                    TTGCGTATGAAGCTGTTATACCTTGAAATAGAGTTGGCCTGGCTAAACTCCTTTTTCCA 1559
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                                                                       772 CCGGAGCAATGCAAGCATTCTCTCAAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAA 831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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STREET: 3054 Cormuallis Road
CITY: Research Triangle Park
STATE: No. 6031153th Carolina
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APPLICANT: Friedrich, Leslie
APPLICANT: Uknes, Scott
APPLICANT: Ruess, Wilhelm
APPLICANT: Rauss, Wilhelm
APPLICANT: Knauf-Beiter, Gertrude
APPLICANT: Knauf-Beiter, Gertrude
APPLICANT: Knauf-Beiter, Helmut
APPLICANT: Costendorn
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,378
FILING DATE: 27-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 13, Application US/08996685
; Patent No. 6031153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                       Score 490; DB 2; Length 1194;
Pred. No. 8.8e-131;
0; Mismatches 410; Indels 15; Gaps
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REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELECOMMUNICATION INFORMATION:
TELEFONE: (919) 541-8689
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1194 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
TOPPLOGY: Linear
MOLECULE TYPE: CDNA
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Best Local Similarity 64.5%;
Matches 771; Conservative 0
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CTHER INFORMATION:
CTHER INFORMATION:
US-08-989-478-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 490; DB 3; Length 11
Pred. No. 8.8e-131;
0; Mismatches 410; Indels
                                                                                                                                                                                                PRIOR PAPELICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/875,015

FILING DATE: 16-010-1997

ATTORNET Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912

TELECOMUNICATION INFORMATION:

TELECHONE: (919) 541-8587

TELEPHONE: (919) 541-8689

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
                                                          FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
       60/034,382
                                              US 60/034,730
                                                                                                                                                                          UMBER: US 60/035,024
10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60 ''
FILING DATE: 10 FILING DATE:
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64.5%;
                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1194 base pairs
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Best Local Similarity 64.5
Matches 771; Conservative
                                                                                                                                            FILING DATE: 10-JAN-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid STRANDEDNESS: single
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OTHER INFORMATION:
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1080 CTACAAATGTTGCTAAGAGAGGGGCATACTACCCTAGATGATGCATATGCTCTCCATTAT 1139
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                              GTCAAGTTGCTTTTGAAAGAGGATCACCAATCTAGATGATGCGTGTGCTCTTCATTTC 531
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APPLICANT: Hunt, Michelle
APPLICANT: Hunt, Michelle
APPLICANT: Hunt, Michelle
APPLICANT: Hunt, Michelle
APPLICANT: Steiner, Henry-York
APPLICANT: Steiner, John
TITLE OF INVENTION: ALTERED FORMS OF THE NIMI GENE CONFERRING
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: No. 5986082artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 5986082th Carolina COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08989478 Patent No. 5986082 GENERAL INFORMATION:
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Tue Oct

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1518 TACCTTGAAAATAGAGTT 1535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              475 CGGTGCACCGGTGCATTTTGTCGCGCGAGGAGTCCGTTCTTTAAGAATTTGTTCTGCGGTA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----AAGGTGGAATTGAAGGAGGTGA 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(2787..3347, 3427..4162, 4271..4474, 4586..4866)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 5655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: /product~ "1st exon of NIM1" FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: exon
LOCATION: 4271..4474
OTHER INFORMATION: /product= "3rd exon of NIM1"
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OTHER INFORMATION: /product- "4th exon of NIM1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon of NIM1"
 PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.3e-83;
0; Mismatches 392;
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Pred. No. 1.3
                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 3427..4162
OTHER INFORMATION: /product= "2nd
                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/034,730 FILING DATE: 10-JAN-1997
                              US/08/989,478
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58.6%;
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TELEFAX: (919) 541-8689
INFORMATION FOR SEC ID NO: 1.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      535 AAAAGGAGAAGAATAGTAGT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 5655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                          Meigs, J. Timothy
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Matches 714; Conservative
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                              APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA HYPOTHETICAL: NO
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LOCATION: 2787.
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; LOCATION:
US-08-989-478-1
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1157 4026 3379 CACATTCATGAATATGTTCTTACTTGAGTACTTGTATTTGTATTTCAGAGGCACTTATTG 3438 978 TCACGAGCGGAACTTGGTCTACAAGGGCCTGAAAGCAACGGTTTTCCTGATAAACATGTT 1037 1158 GCAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCTGATATTAATCATCAAAATTCA 1217 AGGGGATACACGGTGCTGCATGTTGCAGCCATGAGGAAAGAGCCTAAAATTGTAGTGTCC 1277 1278 CTTTTAACCAAAGGAGCTAGACCTTCTGATCTGACATCGATGGAAGAAAAGCACTTCAA 1337 TCTCTCAAAGGCCGACTATGTGTAGAATACTAGAGCAAGAAGACAAAACGAGAACAAATT 4086 CTAGGAGAAGCTTCTGTATCTCTTGCTATGCCAGGCGATGATTTGCGTATGAAGCTGTTA 1517 CCTAGAGATGTTCCTCCTCTTTTGCAGTGGCGCCGATGAATTGAAGATGACGCTGCTC 4146 3319 AGATCCCTGAATTAATTACTCTCTATCAGGTAAAACACCCATCTGCATTAAGCTATGGTTA 3378 977 GAGGGGCATACTACCCTAGATGATGCATATGCTCTCCATTATGCTGTAGCGTATTGCGAT 577 IGAAAGAGCAIGAGGIGAGCIAIGAIGCIGIAAATGAGIGIATIGGCITAITIGIATAGIG 798 GATATICITGACAAAACIGCAGCAGACGAIGIAAIGAIGGITITAICIGITGCAAACAIT 1038 AAGAGGATACATAGGGCATTGGATTCTGATGTTGAATTACTACAAATGTTGCTAAGA ATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATATCCCGGAGCAATGCAAGCAT GCTTCGAATGATCGGTTATGCATTGAGATTCTGGAGCAGAAGCAGAAGAGACCCTCTG GTAAAGTTAGGCCTTCACCTAAAGATGTGTGTGTTTGTGTGGACAATGACTGCTCCATG -----TGGTTGACAAGTTTCAGAGACACTACTG 858 TGTGGTAAAGCATGCGAGAGATTGCTTTCAAGCTGCATTGAGATTATTGTCAAGTCTAAT 918 GTTGATATCATAACCCTTGATAAAGCCTTGCCTCATGACATTGTAAAACAAATTACTGAT

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4; 3079 CTAAGAAGGAGAAAGACTCCAACAACACGCCGCGTGAAGCTCGAGCTTAAGGAGATTG 3138 AGATCCCTGAATTAATTACTCTCTATCAGGTAAAACACCATCTGCATTAAGCTATGGTTA 3378 475 CGGTGCACCGGTGCATTTTGTCGCGAGGAGTCCGTTCTTTAAGAATTTGTTCTGCGGTA 534 GTAAAGTTAGGCCTTCACCTAAAGATGTGTGTGTTTGTGTGGGACAATGACTGCTCTCATG 696 415 CGGAGTITGACTACTICGCCGACGCTAAGCTIGTGGTTTCCGGCCCGTGTAAGGAAATIC 474 GTTGATATCATAACCCTTGATAAAGCCTTGCCTCATGACATTGTAAAACAAATTACTGAT 977 TGGCTTGTAGGCCAGCTGTGGCATTCCTGGTTGAGGTTTTGTACACATCATTTACCTTTC 577 IGAAAGAGCATGAGGTGAGCTATGATGCTGTAATGAGTGTATTGGCTTATTTGTATAGTG ------TGGTTGACAAGTTTCAGAGACACCTACTG ------AAGGTGGAATTGAAGGAGGTGA GATATICTIGACAAAACTGCAGCAGACGATGTAATGATGGTTTTATCTGTTGCAAACATT TGTGGTAAAGCATGCGAGAGATTGCTTTCAAGCTGCATTGAGATTATTGTCAAGTCTAAT CDS join(2787..3347, 3427..4162, 4271..4474, 4586..4866) Length 5655; NAME/KEY: exon LOCATION: 4271..4474 OTHER INFORMATION: /product= "3rd exon of NIM1" LOCATION: 2787..3347 OTHER INFORMATION: /product= "1st exon of NIM1" LOCATION: 4586..4866 OTHER INFORMATION: /Product= "4th exon of NIM1" of NIM1" Score 326.8; DB 3; Pred. No. 1.3e-83; 0; Mismatches 392; NAME/KEY: exon LOCATION: 3427..4162 OTHER INFORMATION: /product= "2nd exon 535 AAAAGGAGAAGAATAGTAGT-----TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) 15.0%; ilarity 58.6%; Conservative (single AGATCTCTGAAT - - - - -Local Similarity NAME/KEY: exon NO NAME/KEY: exon STRANDEDNESS: HYPOTHETICAL: ANTI-SENSE: N' FEATURE: ; NAME/KEY: ; LOCATION: US-08-996-685-1 Matches 714; Query Match FEATURE: FEATURE 3319 757 3439 3559 697 697 798 828 3499 918 qq οp δλ δ δ qq δλ Dp QQ qq δy δ Qγ q δλ g Qγ g δy δ qq

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 4586..4866
OTHER INFORMATION: /product= "4th exon of NIM1"
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0; Mismatches
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OTHER INFORMATION: /product= "lst exon
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                                                                                                      1909
APPLICATION NUMBER: US/08/880,179
                                                                 NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 19
TELECOMUNICATION INFORMATION:
TELERAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 2.
SEQUENCE CHARACTERISTICS:
LENGTH: 5655 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                       DNA (genomic)
                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 58.6
Matches 714; Conservative
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OTHER INFORMATION: /
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4586.
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HYPOTHETICAL: NO
                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
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; LOCATION:
US-08-880-179-2
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTGAAA 3726
                                                                                                                                                                               GCAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCTGATATTAATCATCAAAATTCA 1217
                                                                                                                                                                                                                                                        AGGGGATACACGGTGCTGCATGTTGCAGCCATGAGGAAAGAGCCTAAAATTGTAGTGTCC 1277
                                                                                                                                                                                                                                                                                                                                CTTTTAACCAAAGGAGCTAGACCTTCTGATCTGACATCCGATGGAAGAAAAGCACTTCAA 1337
                                                                                                                                                                                                                                                                                                                                                                                                                 3907 CTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGAACCGCACTCATG 3966
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTAGGAGAAGCTTCTGTATCTCTTGCTATGGCAGGCGATGATTTGCGTATGAAGCTGTTA 1517
                    978 TCACGAGCGGAACTTGGTCTACAAGGGCCTGAAAGCAACGGTTTTCCTGATAAACATGTT 1037
                                                                                         AAGAGGATACATAGGGCATTGGATTCTGATGTTGTTGAATTACTACAAATGTTGCTAAGA 1097
                                                                                                                                                              GAGGGGCATACTACCTAGATGATGCATATGCTCTCCATTATGCTGTAGCGTATTGCGAT 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: No. 6091004artis Corporation
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Delaney, Terry
Friedrich, Leslie
Weymann, Kristlanna
Lawton, Kay
Ellis, Daniel
Uknes, Scott
Jesse, Taco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: VOS, Pieter
TITLE OF INVENTION: GE
TITLE OF INVENTION: SI
TITLE OF INVENTION: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 9919;
                                                                                                                                                                                                   Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 326.8; DB 3;
Pred. No. 1.8e-83;
0; Mismatches 392;
                                    ADDRESSEE: No. 6091004artis Corporation
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
COUNTRY: USA
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                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/880,179
                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                    PC-DOS/MS-DOS
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                                                                                                                 ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INPORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9919 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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58.6%;
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Best Local Similarity 58.6
Matches 714; Conservative
                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 800
        NUMBER OF SEQUENCES:
                                                                                                                                                                               OPERATING SYSTEM:
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US-08-880-179-1
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                                                                                                                                                                                                                                                                                                                       GAGGGCCATACTACCCTAGATGATGCATATGCTCTCCATTATGCTGTAGCGTATTGCGAT 1157
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                                                                       3439 GACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTATACTCAAGCTTGCTAATATA
                                                                                                         858 TGTGGTAAAGCATGCGAGAGATTGCTTTCAAGCTGCATTGAGATTATTGTCAAGTCTAAT
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                                             GATATTCTTGACAAAACTGCAGCAGCATGTGAATGATGGTTTTATCTGTTGCAAACATT
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Delaney, Terry
Delaney, Leslie
Friedrich, Leslie
Weymann, Kristianna
Lawron, Kay
Ellis, Daniel
Uknes, Scott
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Sequence 1, Application US/08880179
Patent No. 6091004
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TITLE OF INVENTION: GEI
TITLE OF INVENTION: SIG
TITLE OF INVENTION: IN
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3123 GACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTATACTCAAGCTTGCTAATATA 3064
                                                                  3063 IGTGGTAAAGCTTGTATGAAGCTATTGGATAGATGTAAAGAGATTATTGTCAAGTCTAAT 3004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Unes, Scott
APPLICANT: Hunt, Michelle
APPLICANT: Hunt, Michelle
APPLICANT: Hunt, Michelle
APPLICANT: Stainer, Henry-York
APPLICANT: Ryals, John
TITLE OF INVENTION: ALTERED FORMS OF THE NIMI GENE CONFERRING
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
TORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5986082artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: No. 5986082artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 5986082th Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Application US/08989478 Patent No. 5986082 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-989-478-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 316.2; DB 2;
Pred. No. 4.9e-81;
0; Mismatches 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Meigs, J. Timothy
REGISTRATION UNBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8687
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 15:
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
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/note= "Ankyrin domains of
                                                                                                                   PRICR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRICR APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRICR APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRICR APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRICR APPLICATION NUMBER: US 60/035,021
APPLICATION NUMBER: US 60/035,021
APPLICATION NUMBER: US 60/035,021
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                        APPLICATION NUMBER: US/08/989,478 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.6%;
64.3%;
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches 496; Conservative
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                     SOFTWARE: Patentin Re-
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) LOCATION: 1.786

OTHER INFORMATION: ,

US-08-989-478-15
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1;

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Db Qy

Search completed: October 8, 2002, 01:24:23 Job time: 116.239 secs

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Database : EST:* 1: em_estba:* 2: em_esthum:* 3: em_esthum:* 4: em_esthum:* 5: em_estpl:* 6: em_estpl:* 7: em_estpl:* 8: em_htc:* 9: gb_estl:* 10: gb_est2:* 11: gb_gss:* 12: gb_gss:* 13: em_gss_hum:* 14: em_gss_hum:* 15: em_gss_pl:* 16: em_gss_vrt:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			Match Length DB ID Description	613 0 MULCOOR	n	10 BG124935	10 BE435499	9 AW622846	10 BE432768	10 BG464249	BI210424	9 AW160234	9 AV551266	10 BE493178	12 BH525927	10 BM111027 BM111027	10 BG598808	9 BE023215 RE023215 RE023215 R	9 AW399343	10 BE918569	
•	.	Query	Match Le	23 B	0.0	21.0	18.4	16.3	16.0	14.6	12.0	11.5	10.8	10.7	9.7	9.1	8.8	8.3	7.9	7.7	,
			Score	517 2	1	457	400.6	354.2	348	316.2	261.2	249	234.2	232	211.2	198.2	191.8	179.6	171.8	167.2	771
		Result	No.		,	7	m	c 4	2	ø	7	æ	σ	10	c 11	12	13	14	15	16	17

BH211724 SALK_0065 BF657743 OV2_17_E0 BF657743 OV2_17_E0 BF69790 EST360805 BM307942 SAS13908. BG52676 63-52 Ste B26306 F18D8TF IGF B1968018 GM830068 A1442277 Sa66a04.y AM216501 EST295215 BG526883 40-96 Ste BG52488 10-59 Ste BG52487 10-59 Ste A1372473 HAEA51C01 BE801977 Sr23d08.y AW31082 S431b02.x BE366196 P11_31_F0 BH48357 BGCXP26TF BH48357 BGCXP26TF BM36196 P11_31_F0 BM324012 P11_31_F0 BM324012 P10_30_C AW618718 EST320304 A1960862 SC91f07.y T22612 4650 Lambda BE020423 SM40e088.y AW349633 GM2100066A	ALIGNMENTS AMI60235 BAN160235 EST290093 L. pennellii trichome, Cornell University Lycoperation pennellil CDNA clone cLP7119 similar to A. thaliana transcription pennellil CDNA clone cLP7119 similar to A. thaliana transcription AMI60235. GI:6279769 EST. Lycopersicon pennellii. Lycopersicon lycopersicon pennellii.
BH211724 BF657743 BR1096790 BN107942 BGA144779 BG144277 AW216501 BG526681 BG526881 BG52681 BG52681 BG52677 AW310982 BE36197 AW310982 BE36197 AW310982 AW684759 AW3109867	AMIGO235 BAN160235 EST290093 L. pennellii trichome, Corn pennelli CDNA clone cLPTI19 similar factor inhibitor I kappa B homolog, m AWI60235 GI:6279769 EST. Lycopersicon pennellii. Lycopersicon loopiya. Wajnolophyta; watlaca, J. Vrebalov, J. White, R. Matland, F. Hansen, T. S. Upton, J. Ronn C.X.Y. Bowman, C.L., Nierman, W., Frase, J. Tanksley, S. D. and Giovannoni, J Generation of ESTs from wild tomato (trichomes Contact: CUGI Clemson University Genomics Institute Clemson University Acquanism-Lycopersicon penn Abarref-Taxon: 28526" Actione-Clemson
	annelli clone o br I kap i kap clone o concelli annell
5 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	AW160235 EST290093 L. pennellii tricipennellii cDNA clone cLPTLICIPENTOLIONALIONE CLPTLICIPENTOLIONALIONE CLPTLICIPENTOLIONALIONELLA AW160235. IG:6279769 EST. Lycopersicon pennellii. Lycopersicon. Lycopersicon. Lycopersicon. Lycopersicon. Lycopersicon. Cases 1 to 613 Alcala, J. Vrebalov, J., Whittliang, F., Hansen, T.S., Upton, C.Y., Bowman, C.L., Nierman, C.L., Nierman, C.L., Nierman, C.L., Nierman, C.L., Nierman, C.L., Nierman, C.B., Tanksley, S.D. and Glogentarion of ESTS from wild Generation of ESTS from wild Clemson University Genomics Clemson University Genomics Clemson University Genomics Clemson University Genomics Clemson University Location/Qualifiers Jorganism="Lycopers" Alb., nost="Lorplip" Clone="Lorplip" Alb., nost="Lorplip" Alb., nost="Nector: pBlux" Anot="Vector: pBlux" Anot="Nector: pBlux" Anota-"Anota-"Coller Anota-"Anota-"Anota-"Coller Anota-"Ano
	AW160235 EST290093 L. pe EST290093 L. pe EST290093 L. DE AW160235 G.
163.6 162.6 11.6 115.6 1152.6 1150.2 1146.7 1146.7 1128.4 1128.4 1128.6 1128.6 1128.6 1128.6 1128.6 1128.6 1128.6 1128.6 1128.6 1128.6 1139.6 110.8 1110.8 1110.8 1110.8	AW16023 EST29000 pennell. factor AW16023 AW16023 AW16023 AW16023 EST. Lycopers Contact: Conta
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Unpublished (2001)
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Best Local 9
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ORIGIN
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Matches
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COMMENT
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nitrogen, shearing off trichomes. This procedure yielded a mixture of cells highly enriched for trichomes, with minor contamination by other types of leaf cells."
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 654)
van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T.,
Hansen,C., Ronning,C. and Tanksley,S.
Generation of ESTs from tomato shoot/meristem tissue
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                                                                                                                                                                                      AGGCGATGATTTGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTGGCCTGGCTAAACT 1549
                                                                                                                                                                                                                                        CCTTTTTCCAATGGAAGCTAAAGTTGCAATGGACATTGCTCAAGTTGATGGCACTTCTGA 1609
                                                                                                                                                                                                                                                                                           GTTCCCACTGGCTAGCATCGGCAAAAAGATGGCTAATGCACAGAGGACAACAGTAGATTT 1669
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                                                                                                                                     1430 GGAGCAAGCAGAAAGAAGAGCCCTCTGCTAGGAGAAGCTTCTGTATCTCTTGCTATGGC 1489
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                                                                                                                                                                                                                                                                                                         GGATGCTGATGACTTGTCTGAGATAGCTTACATGGGGAATGATACGGCAGAAGAGCGTCA
                                                                                                               4
                                                                                  Length 613;
                                                                                                             Indels
                                                                                                             38;
                                                                                 Score 517.2; DB 9;
Pred. No. 9.1e-104;
0; Mismatches 38;
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BG124935
BG124935.1 GI:12625123
                                                                                    23.8%;
93.1%;
                                                                                                   Best Local Similarity 93.1
Matches 564; Conservative
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DEFINITION
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KEYWORDS
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BG124935
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/note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2: Xhol: Small expanding leaves from the growing tip were taken from greenhouse plants (4-6wks old TA496). Tissue was immediately frozen in liquid nitrogen."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1557 CCAATGGAAGCTAAAGTTGCAATGGACATTGCTCAAGTTGATGGCACTTCTGAGTTCCCA 1616
                                                                                                              /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="crOF7K1"
/clone="Lype="shoot/meristem"
/tissue_type="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
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Contact: Cugi
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                        Length 654;
                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                           50;
                                                                                                                                                                                                                                                                                                                                                                        Score 457; DB 10;
Pred. No. 1.8e-90;
0; Mismatches 50;
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88.0%;
                                                                                                                                                                                                                                                                                                                                                                                                               552; Conservative
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l (bases I to 516)
van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang
.F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W.,
Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
Generation of ESTs from tomato flower tissue, 3-8 mm buds
Contact: CUGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 18-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Lycopersion esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="crobs42"
/clone="trobs42"
/clone_lib="tomato flower buds 3-8 mm, Cornell University"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lycopersicon esculentum
Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="flower"
/dev_stage="3-8mm buds"
/dev_stage="3-8mm buds"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1609 AGTICCCACTGGCTAGCATCGGCAAAAAGATGGCTAATGCACAGAGGACAACAGTAGATT 1668
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                                                                          726
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                                                                                           787 GACACCTACTGGATATTCTTGACAAAACTGCAGCAGACGATGTAATGATGGTTTTATCTG
                                                                                                                                                                                                                                                       449 TGGTCAGTGTCGCCTATTTGTATAGTGGAAAAGTTAGGCCTGCATCTAAAGATGTGT
                                                                      GTGTTTGTGTGGACAATGACTGCTCTCATGTGGCCTTGTAGGCCAGCTGTGGCATTCCTGG
                                                                                                                                                 727 TTGAGGTTTTGTACACATCATTTACCTTTCAGATCTCTGAATTGGTTGACAAGTTTCAGA
          4 ;
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clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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                                                                                                                                                                                                                                                                                                                                    Score 354.2; DB 9;
Pred. No. 8.6e-68;
0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                 TTGCAAACATTTGTGGTAAAGCATGCGAGAGATTGCTTTCA
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92.5%;
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395; Conservative
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                     BE435499 736 bp mRNA linear EST 18-MAY-2001 EST406577 tomato breaker fruit, TICR Lycopersicon esculentum cDNA clone cLEG27M10, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of
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Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
                                                                                                                                                              Lycopersicon esculentum Streptophyta; Embryophyta; Tracheophyta; Sukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBluescriptSKmCUadapt; Site_1: EcoRl; Site_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 ATAGTAGGACTGCGTTTTCTGATTCGAATGACATCAGCGGAAGCAGTAGTATATGCTGCA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367 IGAAACGCCTATCGGAAACACTGGAATCTATCTTCGATGCGTCTTTGCCGGAGTTTGACT 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGCCGCCGCCATGACTTTTTCTCGCCGGAGACTTCGCCGGCGGAGATCACTTCAC 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     547 ATAGTAGTAAGGTGGAATTGAAGGAGGTGATGAAAGAGCATGAGGTGAGCTATGATGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Generation of ESTs from tomato fruit tissue, breaker stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTICGCCGACGCTAAGCTTGTGGTTTCCGGCCCGTGTAAGGAAATTCCGGTGCACCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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Pred. No. 4.9e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="clbg27M10"
/clone_lib="tomato breaker fruit, TIGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Lycopersicon esculentum"/cultivar="TA496"
/db_xref="taxon:4081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                  BE435499.1 GI:9433342
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                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: CUGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prime sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Enliopsida; Poales; Poaceae; PACC clade; Panicolaeae; Andropogoneae; Sorghum.

E 1 (bases 1 to 614)
S Reid,S.P., Cordonnier-Pratt,M.-M., Gingle,A. and Pratt,L.H.
An EST database from Sorghum: developing embryos
L Unpublished (2000)
Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG464249 614 bp mRNA linear EST 20-MAR-2001 EML_71_D12.b1_A002 Embryo 1 (EM1) Sorghum bicolor cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to exclude PolyA, vector and regions threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                         TCTTCGATGCGTCTTTGCCGGAGTTTGACTACTTCGCCGACGCTAAGCTTGTGGTTTCCG 456
                                                                                                                                                                                                                126 GC---GGTAAGGAAATTCCGGTGCATCGGTGCATTTTGTCGGCGAGGAGTCCTTTTTTA 182
                                                                                                                                                                                                                                                                  AGAATTTGTTCTGCGGTAAAAGGAGAAATAGTAGTAAGTGGAATTGAAGGAGGTGA 576
                                                                                                                                                                                                                                                                                                                                                         TGGCTTGTAGGCCAGCTGTGGCATTCCTGGTTGAGGTTTTGTACACATCATTTACCTTTC 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGAGACTICGCCGGCGGAGATCACTTCACTGAAACGCCTATCGGAAACACTGGAATCTA 396
                  Gaps
                                                                            6 CGGAAACTTCACTGGCAGACGTCAATTCCCTCAAACGTCTATCAGAAACACTAGGAGTCTA 65
                                                                                                                                                                                                                                                                                      GCCCGTGTAAGGAAATTCCGGTGCACCGGTGCATTTTGTCGGCGAGGAGTCCGTTTTA
                                                                                                                                                                                                                                                                                                                                      TGAAAGAGCATGAGGTGAGCTATGATGCTGTAATGAGTGTATTGGCTTATTTGTATAGTG
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                  Indels
              16;
                Mismatches
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   Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
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High quality sequence stop:
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83.28;
   Similarity 83.2 2; Conservative
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Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Glovannoni,J.J. and Tanksley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               503 bp mRNA linear EST 18-MAY-200
ST399297 tomato breaker fruit, TIGR Lycopersicon esculentum CDNA
CLONE CLEGIOA24, mRNA sequence.
                                                                                                                                                                                                                                                                                                                             2028
                                        1788
                                                                                                             1789 TGGATGCTGATGACTTGTCTGAGATAGCTTACATGGGGAATGATACGGCAGAAGAGCGTC 1848
                                                                                                                                                                                  1849 AACTGAAGAAGCAAAGGTACATGGAACTTCAAGAAATTCTGACTAAAAGCATTCACTGAGG 1908
                                                                                                                                                                                                                                                       ATAAAGAAGAATATGATAAGACTAACAACATCTCCTCCTCTTGTTCCTCTACATCTAAGG 1968
                                                                                                                                                                                                                                                                         337
                                                                                                                                                277
                                                                                                                                                                                                                                                                                                                                                1969 GAGTAGATAAGCCCAATAAGCTCCCTTTTAGGAAATAGGTAATTGTATTAGGATATATAGA
                                        GAACTGTAGAACTTGGAAAACGCTTCTTTCCACGTTGTTCAGAAGTTCTAAATAAGATCA
                                                           Generation of ESTs from tomato fruit tissue, breaker stage Unpublished (2000)
Contact: CUGI
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="cLEGI0A24"
/clone_lib="tomato breaker fruit, TIGR"
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
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1. .503
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                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAAGAA 94
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AUTHORS
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//note—Vector: Bluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Suspension cultures of L.esculentum E6203 were grown
in Murashige and Skoog based medium, supplemented with 15%
coconut milk (filter sterilized and added after
autoclaving), 2% saccharose, and Img/ml 2,40 (pH5.8).
Fresh medium was added every 7 days, and cultures were
grown at 25 C, with 12hrs of light and continuous
shaking."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 18-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST290092 L. pennellii trichome, Cornell University Lycopersicon pennellii cDNA clone cLPT119, mRNA sequence.
1 (bases 1 to 539)
van der Hoeven, R., Sun, H., Bezzerides, J., Cho, J., Utterback, R., Ronning, C. and Tanksley, S.
Generation of ESTs from Tomato Suspension Cultures
Uppublished (2001)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1724 CICTAGAACTGTAGAACTTGGAAAACGCTTCTTTCCACGTTGTTCAGAAGTTCTAAATAA 1783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1784 GATCATGGATGCTGATGACTTGTCTGAGATAGCTTACATGGGGAATGATACGGCAGAAGA 1843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1903 1844 GCGTCAACTGAAGAAAGGTACATGGAACTTCAAGAATTCTGACTAAAGCATTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1904 TGAGGATAAAGAAGAATATGATAAGACTAACAACATCTCCTCTTGTTCCTCTACATC 1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAAGGGAGTAGATAAGCCCCAATAAGCTCCCTTTTAGGAAATAGGTAATTGTATTAGGATA 2023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2084 TCAACATACATACAACAGCTGTACCATAAACTTGTATTGTTGCACTTACAACTTTGAAGA 2143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 TATGAGGAAGAAACACCAGGACTCTTTTTTTT----TTTCATCATTTGATGCATACAAAAC 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                353 ACATGTACCATAAACTTGTATTGTGAAAAAAAAAAATTTCATTATTAGTTGAGAAGC 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 539;
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                                                                                                                                                                                                                                                            esculentum"
                                                                                                                                                                                                                                                                                                                                                             /tissue_type="suspension cultures"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.0%; Score 261.2; DB 78.6%; Pred. No. 2.9e-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                      /organism="Lycopersicon e
/cultivar="TA496, E6203"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:4081"
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                                                                                                                                                                                                                                                                                                                  /clone="cTOS23C4"
/clone_lib="cTOS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     shaking."
77 c
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                                                                TITLE
JOURNAL
COMMENT
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                              AUTHORS
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        REFERENCE
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               /clone_lib="Embryo 1 (EM1)"
/note="Organ: Embryos germinated for 24 hr; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
EcoRI; The library was made from poly-A RNA in the cloning
vector lambda Zap II. Clones to be sequenced were
                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BI210424 539 bp mRNA linear EST 11-JUL-2001 EST528464 CTOS Lycopersicon esculentum CDNA clone cTOS23C4 5' end,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                        996 CTACAAGGCCCTGAAAGCAACGGTTTTCCTGATAAACATGTTAAGAGGATACATAGGGCA 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1056 ITGGATTCTGATGATGTTGAATTACTACAAATGTTGCTAAGAGAGGGGCATACTACCTA 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1116 GATGATGCATATGCTCTCCATTATGCTGTAGCGTATTGCGATGCAAAGACTACAGCAGAA 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITCIAGAICTIGCACTIGCTGAIATTAATCATCAAAATTCAAGGGGATACACGGTGCTG 1235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1296 AGACCTICTGATCTGACATCCGATGGAAGAAAGCACTTCAAATCGCCAAGAGGCTCACT 1355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1476 TCTCTTGCTATGGCAGGCGATGATTTGCGTATGAAGCTGTTATACCTTGAAAATAGAGTT 1535
                                                                                                                                                                                                                                                                                                                                                                                                  187
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                                                                                                                                                                                                                                                                                                                               8 GAGAAGGCATTGCCTCCAGATGTTGTCAAAGCAATTGTTGATGCAAGGCTAAGTCTTGGA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                936 GATAAAGCCTTGCCTCATGACATTGTAAAACAAATTACTGATTCACGAGCGGAACTTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó,
                                                                                                                                                                                                               Length 614;
                                                                                                                                                                                                        Score 316.2; DB 10; Length
Pred. No. 2.1e-59;
0; Mismatches 178; Indels
                                                                                                                        prepared by mass excision."
125 c 146 g 155 t
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                                                                                                                                                                                                        Query Match
Best Local Similarity 70.4%;
Matches 423; Conservative
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BI210424
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BI210424
LOCUS
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519 GIGTITGIGIGGACAAIGAGIGCIIGCAIGIAGCIIGIA 557

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Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 573)
Asamizu.E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
                                                                                        EST 06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The First Laboratory for plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizuékazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                            AV551266 Arabidopsis thaliana roots Columbia Arabidopsis thaliana conts Columbia Arabidopsis thaliana conts Columbia Arabidopsis thaliana conta clone RZ123e05R 5', mRNA sequence.
AV551266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="roots"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATAAACATGTTAAGAGGATACATAGGGCATTGGATTCTGATGATGTTGAATTACTACAAA 1086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGTAGTGTCCCTTTTAACCAAAGGAGCTAGACCTTCTGATCTGACATCCGATGGAAGAA 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    967 AAATTACTGATTCACGAGCGGAACTTGGTCTACAAGGGCCTGAAAGCAAGGTTTTCCTG 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGTATTGCGATGCAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCTGATATTAATC 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               907 TCAAGICTAATGTIGATATCATAACCCTIGATAAAGCCTTGCCTCAIGACATTGTAAAAC 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1087 IGTIGCTAAGAGGGGCATACTACCCTAGATGATGCATATGCTCTCCATTATGCTGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 IGCITITGAAAGAGGATCACACCAATCIAGATGATGCGTGTGCTCTTCATITCGCTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Arabidopsis thaliana roots Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AGATAATTGATAGACGTAAAGAGCTTGGTTTGGAGGTACCTAAAGTAAAG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 234.2; DB 9;
Pred. No. 2.6e-41;
); Mismatches 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. 573
/organism="Arabidopsis thaliana"
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                                                                                          573 bp
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/db_xref="taxon:3702"
/clone="R2123e05R"
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                                                                                                                                                                            AV551266.1 GI:8722679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Erika Asamizu
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ilarity 64.1%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 c
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Matches 375;
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                                                                                                                  DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Leaves of various stages were shaken in liquid nitrogen, shearing off trichomes. This procedure yielded a mixture of cells highly enriched for trichomes, with minor contamination by other types of leaf cells."
                                                                                                                                                                                Holt, I.E.,
B., Fujii
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                                                                           Eŭkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                             I (bases I to 557)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Lakey,J., Holt,I.E. Lang,F., Hansen,T.S., Upton,J., Ronning,C.M., Craven,M.B., Fujli,C.Y., Eowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from wild tomato (Lycopersicon pennellii)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cornell University"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 ATAGTAGAACTGCTTTTTCGGATTCCAATGATATTAGTGGAAGCAGTAGTATATGCTGCA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCGGCGGCGCCATGACTGAATTTTTCTCGCCGGAGACTTCGCCGGCGGAGATCACTTCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAAACGCCTATCGGAAACACTGGAATCTATCTTCGATGCGTCTTTGCCGGAGTTTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 TCAAACGTCTATCAGAAACACTAGAGTCTATCGATGCGTCTGCGCCGGATTTCGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCATTTTGTCGGCGAGGAGTCCGTTCTTTAAGAATTTGTTCTGCGGTAAAAAGGAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                345 GCATTTTGTCGGCGAGGAGTCCTTTTTTAAGAATGTATTCTGTGGGAAA-----GATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            547 ATAGTAGTAAGGTGGAATTGAAGGAGGTGATGAAAGAGCATGAGGTGAGCTATGATGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            399 GCAACACGAAGCTGGAACTCAAAGAGCTGATGAAGAGTATGAGGTGAGTTTTGATGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30;
                                                                                                                                                                                                                                                                                                                            Confact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Lycopersicon pennellii"
/db_xref="taxon:28526"
/clone="cLPT119"
/clone=lb="L, pennellii trichome, ''/tissue_type="trichome"
/dev_stage="mixed stages"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.5%; Score 249; DB 9; Lalarity 77.1%; Pred. No. 1.4e-44; Conservative 0; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIGITIGIGIGACAAIGACIGCICICAIGIGGCIIGIA 705
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  GI:6279768
                                           Lycopersicon pennellii
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Unpublished (1999)
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                                                                Lycopersicon
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nes 354; Conserv
AW160234.1
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                                                                                                                                                                 REFERENCE
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GSS 13-DEC-2001
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Brusaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                               953 TGACATTGTAAAACAAATTACTGATTCACGAGCGGAACTTGGTCTACAAGGGCCTGAAAG 1012
                                                                                                                                                                                                                                                                                                                                                               1073 IGAATTACTACAAATGTTGCTAAGAGGGGGCATACTACCTAGATGATGCATATGCTCT 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1133 CCATTATGCTGTAGCGTATTGCGATGCAAAGACTACAGGCAGAACTTCTAGATCTTGCACT 1192
                                                                                                                                                                                                                                               .013 CAACGGTTTTCCTGATAAACATGTTAAGAGGATACATAGGGCATTGGATTCTGATGATGT 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCTGATATTAATCATCAAAATTCAAGGGGATACACGGTGCTGCATGTTGCAGCCATGAG 1252
                                                                                                                                                                                                                                                                                128 AGAIGTTATCAAGCAAATTATTGATTCACGGATAACTCTTGGATTAGCTTCACCGGAAGA 187
                                                                                                                                                                                                                                                                                                                                                                                                248 GGAGCTTGTCAGGATGCTGCTCACAGAAGGCAGACTAAACCTTGATGATGCATTTGCATT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       893 CATTGAGATTATTGTCAAGTCTAATGTTGATATCATAACCCTTGATAAAGCCTTGCCTCA 952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BH525927 772 bp DNA linear GSS 13-E
BOGTO04TF BOGT Brassica oleracea genomic clone BOGTO04, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 GCACTATGCTGTAGAACACTGTGACTCTAAAAATTACAACAGAACTTCTGGACATGGCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Tol000BH3"
/db.xref="texon:3712"
/clone="BGGT004"
/clone_lib="BGGT"
/clone_lib="BGGT"
/note="Vector: pHoS1; Site_1: BstX1; 2-3 kb
genomic DNA inserted into pHoS1 using BstX1
1 187 c 176 g 210 t
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Town.C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other_GSSS: BOGTO04TR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9712 Medical Center Drive, Rockville, MD 20850,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.7%; Score 211.2; DB 12;
61.0%; Pred. No. 3.1e-36;
tive 0; Mismatches 223;
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1. 772
/organism="Brassica oleracea"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               428 GAGAGATCCTAAAATTGTTGTCTTCCTT 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 61.09
Matches 367; Conservative
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Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida: Poales; Poaceae; Pooideae; Triticeae; Triticaeae; Triticaeae; Triticaeae; Triticaeae; Triticeae; Triti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2001)

Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Vegetative shoot apex"
/dev_stage="Three weeks-old plants"
/dab_bost="E. coli XLOLR"
/nab_bost="E. coli XLOLR"
/note="Vector: Lambda pBK-CMV (Lambda Zap Express),
excised phagemid; Site_1: EcoRI; Site_2: XhoI; The tissue,
total RNA, and poly(A) RNA were prepared, a cDNA library
was made, and the cDNA clones were in vivo excised at the
University of California, Davis (V. Echenique, B. Stamova
'J. Dubcovsky). Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE493178
WHE0570_C11_F222E Triticum monococcum vegetative apex cDNA library
Triticum monococcum cDNA clone WHE0570_C11_F22, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
1327 AAGCACTTCAAATCGCCAAGAGGCTCACTAGGCTTGTGGATTTCAGTAAGTCTCCGGAGG 1386
                                                                                                                      AAGGAAAATCTGCTTCGAATGATCGCTTATGCATTGAGATTCTGGAGCAAGGAAAGAA 1446
                                                                                                                                                 409 CCGCACTCATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATATATCCCGGAGC 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Triticum monococcum"
/cultivar="DV92"
/db_xref="taxon:4568"
/clone="WHF0570_cll_F22"
/clone="Ith="Triticum monococcum vegetative apex cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene T3 primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                    Pred. No. 8.1e-41;
0; Mismatches 135;
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/db_xref="taxon:4113"
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ilarity 60.5%;
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1 (bases 1 to 700)
wan der Hoeven, N., Sun, H., Karamycheva, S. A., Tsai, J., Van Aken, S., Utterback, T., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.
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                                                                                                   CATTGGATTCTGATGATGTTGAATTACTACAAATGTTGCTAAGAGAGGGGCATACTACCC 1113
                                                                                                                                                             1114 TAGATGATGCATATGCTCTCCATTATGCTGTAGCGTATTGCGATGCAAAGACTACAGCAG 1173
                                                                                                                                                                                                                    AACTICIAGAICTIGCACTIGCTGATATIAAICATCAAAATICAAGGGGATACACGGTGC 1233
                                                                                                                                                                                                                                                                              TGCATGTTGCAGCCATGAGGAAAGAGCCTAAAATTGTAGTGTCCCTTTTAACCAAAGGAG 1293
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                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Research Genetics, Libraries Division
Tel: 1-800-711-6195
Email: cdna@resgen.com
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                CTAGGCTTGTGGATTTCAGTAAGTCTCCGGAGGAAGGAAAATCTGCTTCGAATGATCGGT
                                                                       712 GTCTCGAGCCGCCCGA------GCCGGATAAACATGTCATGAACATATACAAGG
                                                                                                                    GTCTACAAGGGCCTGAAAGCAACGGTTTTCCTGATAAACATGTTAAGAGGATACATAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cultivar≂"Kennebec"
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Solanum tuberosum
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BM111027
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AUTHORS
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/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Cornell University, Tanksley lab; sequencing: The Institute for Genomic Research. Roots were isolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium."
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

[ (pases 1 to 667)
van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A.,
Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.
Generations of ESTs from sprouting potato eyes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITCCIGATAAACAIGITAAGAGGATACATAGGGCATIGGATTCTGATGATGTTGAATTA 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1080 CTACAAATGTTGCTAAGAGGGGCATACTACCCTAGATGATGCATATGCTCCCATTAT 1139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1200 ATTAATCATCAAAATTCAAGGGGATACACGGTGCTGCATGTTGCAGCCATGAGGAAAGAG 1259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221 GTCAAGCTTCTACTTAATGAGTCTGACATAAGTTTAGATGGAGCCTACGCTCTTCATTAC 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       581 ATGCGTCACAACCCAATGACCGGAGATGCATTATTTTCTTCCCCCATGTTGGCCGATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                            Length 700;
/clone="cPR010C3"
/clone_lib="potato roots"
/tissue_type="roots"
/dev_stage="in vitro grown stem cuttings"
                                                                                                                                                                                                                                                                                                                                                                                                   Score 198.2; DB 10; Length
Pred. No. 2.3e-33;
0; Mismatches 213; Indels
                                                                                                                         /lab_host-"SOLR"
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BG598808.1 GI:13618649
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JOURNAL

COMMENT

source

FEATURES

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'Supernod' plants generoually donated by Dr. Gary Stacey.
The seedlings were innoculated with Bradyrhizobium
japonicus, strain USDAILO priot to harvest. Stratagene's
cDNA synthesis Kit (catalog number 200401) was used to
synthesize the cDNA. First-strand synthesis was performed
with Smethyl dCTP, hence the ligated CDNA was
hemimethylated. A modification of Stratagene's
first-strand synthesis primer was used. An 'anchor'
nucleotide (V-A.C. or G) was added to the 3' end of the
primer [GAGAGAGAGAGAGAACARGTCTCGAG[T]]8V] to anchor
the primer at the 5' end of the poly(A) tract. After
second-strand synthesis, the cDNA ends were filled in with
cloned Pfu DNA polymerase, ligated to EcoRI adapters and
subsequently phosphorylated. The XhoI site within the
first-strand synthesis primer was then restricted by
digestion with XhoI; all XhoI sites in the cDNA
constructs were size-fractionated with a 500bp cutoff,
using GibcoBRL Life Technologies' cDNA size Fractionation
Stratagene's splauescript II XR predigested with EcoRI
and XhoI, and phosporylated by Stratagene's Both the
white and blue colonies appear to contain recombinant
plasmids with CDNA inserts, based on size (n=25). This
library was constructed by Dr. Paul Keim and Dr. Virginia
Corpeal."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 contact via email: ccu@resgen.com
sm70a04.yl Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1028-9223 5' similar to TR:081848 081848 HYPOTHETICAL 68.2 KD
PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                           Shoemaker, R. Kehin, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptco, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Kitter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, Public Soybean EST Project
Unpublished (1999)
Public Soybean EST Project
Public Soybean EST Project
                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; The mRNA was isolated from roots of Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1028-9223"
/clone_lib="Gm-c1028"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="roots of 'Supernod' plants"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                            DEFINITION
                                                                                                                                                                                                                             ORGANISM
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                           ACCESSION
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the frozen for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1203 AATCATCAAAATTCAAGGGGATACACGGTGCTGCATGTTGCAGCCATGAGGAAAGAGCCT 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1263 AAAATTGTAGTGTCCCTTTTAACCAAAGGAGCTAGACCTTCTGATCTGACATCCGATGGA 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1503 CGTATGAAGCTGTTATACCTTGAAAATAGAGTTGGCCTGGCTAAACTCCTTTTTTCCAATG 1562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1086 ATGTTGCTAAGAGAGGGGCATACTACCCTAGATGATGCATATGCTCTCCATTATGCTGTA 1145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          422 ATTAGGAATCCTATGATTGGGAGCATGTCTTCTTCATCATTGGTGTTGGTGATTA 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 667;
                                                                                                                                                                                                                                                                                                                                                                                          from tubers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1563 GAAGCTAAAGTTGCAATGGACATTGCTCAAGTTGATGGCACTTCTGA 1609
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/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
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                                                                                                                                                                                                                                              /organism="Solanum tuberosum"/cultivar="Kennebec"
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Pred. No. 6e-32;
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/clone="cSTS22E2"
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                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                  Seg primer: M13F-R.
                                 Unpublished (2000)
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Query Match Local

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BASE COUNT

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BE023215

RESULT 14 BE023215 LOCUS

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AW399343 450 bp mRNA linear EST 18-MAY-2001 EST309843 L. pennellii trichome, Cornell University Lycopersicon pennellii cDNA clone cLPT7013 5', mRNA sequence.
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Lakey,J., Holt,I.E.
Liang,F., Hanseh,T.S., Upton,J., Ronning,C.M., Craven,M.B., Fujii
,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin
,G.B., Tanksley,S.D. and Glovannoni,J.
Generation of ESTs from wild tomato (Lycopersicon pennellii)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lycopersicon pennellii
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                      1335
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/tissue_type="trichome"
/dev_stage="mixed stages"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1036 TTAAGAGGATACATAGGGCATTGGATTCTGATGATGTTGAATTACTACAAATGTTGCTAA 1095
                                                                                                                                                       1096 GAGAGGGGCATACTACCCTAGATGATGCATATGCTCTCCATTATGCTGTAGGGTATTGCG 1155
                                                                                                                                                                                                                                 1156 ATGCAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCTGATATTAATCATCAAAATT 1215
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                                                                                               1276 CCCTTTTAACCAAAGGAGCTAGACCTTCTGATCTGACATCCGATGGAAGAAAAGCACTTC
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
 Length 458;
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/organism="Lycopersicon pennellii"
/db_xref="taxon:28526"
/clone="cLPT7013"
Score 179.6; DB 9;
                                     165;
                 3e-29;
                                   0; Mismatches
                     Pred. No.
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AW399343.1 GI:6917813
8.3%;
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                                     278; Conservative
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AW399343
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AUTHORS
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Leaves of various stages were shaken in liquid
nitrogen, shearing off trichomes. This procedure yielded a
mixture of cells highly enriched for trichomes, with minor
contamination by other types of leaf cells."
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                                                                                                                                                                                                                                        1041 AGGATACATAGGGCATTGGATTCTGATGATGTTGAATTACTACAAATGTTGCTAAGAGAG 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1221 GGATACACGGTGCTGCTGCTTGCAGCCATGAGGAAAGAGCCTAAAATTGTAGTGTCCCTT 1280
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                                                                                                                                                                                                                                                                                                                                       TCTGACATAAGTTTAGATGGAGCCTACGCTCTTCATTACGCTGTTGCATATTGTGAGACCCC
                                                                                                                                                                                                                                                             2 AGGATATACAAGGCATTGGATTCGGATGATGTTGAACTTGTCAAGCTTTTACTTAATGAG
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                                                                                                                                                                                                     ;
0
                                                                                                                                                                Length 450;
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                                                                                                                                                            Score 171.8; DB 9;
Pred. No. 1.6e-27;
0; Mismatches 172;
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                                                                                                                                                                Similarity 61.5%; 5; Conservative (
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Job time: 1710.05 secs
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Best Local $
                                                                                                            BASE COUNT
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                                                                                                                                                                                                         Matches
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